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(54) Title: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

(57) Abstract: Disclosed herein are nucleic acid sequences that encode novel polypeptides. Also disclosed are polypeptides encoded by these nucleic acid sequences, and antibodies, which immunospecifically-bind to the polypeptide, as well as derivatives, variants, mutants, or fragments of the aforementioned polypeptide, polynucleotide, or antibody. The invention further discloses therapeutic, diagnostic and research methods for diagnosis, treatment, and prevention of disorders involving any one of these novel human nucleic acids and proteins.

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NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

BACKGROUND OF THE INVENTION

The invention generally relates to nucleic acids and polypeptides. More particularly, the invention relates to nucleic acids encoding novel molecule (MOL) polypeptides, as well as
5 vectors, host cells, antibodies, and recombinant methods for producing these nucleic acids and polypeptides.

SUMMARY OF THE INVENTION

The invention is based in part upon the discovery of nucleic acid sequences encoding novel polypeptides. The novel nucleic acids and polypeptides are referred to herein as
10 MOLX, or MOL1, MOL2, MOL3, MOL4, MOL5, MOL6, MOL7, and MOL8 nucleic acids and polypeptides. These nucleic acids and polypeptides, as well as derivatives, homologs, analogs and fragments thereof, will hereinafter be collectively designated as "MOLX" nucleic acid or polypeptide sequences.

In one aspect, the invention provides an isolated MOLX nucleic acid molecule
15 encoding a MOLX polypeptide that includes a nucleic acid sequence that has identity to the nucleic acids disclosed in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23. In some embodiments, the MOLX nucleic acid molecule will hybridize under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule that includes a protein-coding sequence of a MOLX nucleic acid sequence. The invention also includes an isolated
20 nucleic acid that encodes a MOLX polypeptide, or a fragment, homolog, analog or derivative thereof. For example, the nucleic acid can encode a polypeptide at least 80% identical to a polypeptide comprising the amino acid sequences of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24. The nucleic acid can be, for example, a genomic DNA fragment or a cDNA molecule that includes the nucleic acid sequence of any of SEQ ID NOS:1, 3, 5, 7, 9,
25 11, 13, 15, 17, 19, 21, and 23.

Also included in the invention is an oligonucleotide, *e.g.*, an oligonucleotide which includes at least 6 contiguous nucleotides of a MOLX nucleic acid (*e.g.*, SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23) or a complement of said oligonucleotide.

Also included in the invention are substantially purified MOLX polypeptides (SEQ ID
30 NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24). In certain embodiments, the MOLX

polypeptides include an amino acid sequence that is substantially identical to the amino acid sequence of a human MOLX polypeptide.

The invention also features antibodies that immunoselectively bind to MOLX polypeptides, or fragments, homologs, analogs or derivatives thereof.

5 In another aspect, the invention includes pharmaceutical compositions that include therapeutically- or prophylactically-effective amounts of a therapeutic and a pharmaceutically-acceptable carrier. The therapeutic can be, *e.g.*, a MOLX nucleic acid, a MOLX polypeptide, or an antibody specific for a MOLX polypeptide. In a further aspect, the invention includes, in one or more containers, a therapeutically- or prophylactically-effective amount of this
10 pharmaceutical composition.

In a further aspect, the invention includes a method of producing a polypeptide by culturing a cell that includes a MOLX nucleic acid, under conditions allowing for expression of the MOLX polypeptide encoded by the DNA. If desired, the MOLX polypeptide can then be recovered.

15 In another aspect, the invention includes a method of detecting the presence of a MOLX polypeptide in a sample. In the method, a sample is contacted with a compound that selectively binds to the polypeptide under conditions allowing for formation of a complex between the polypeptide and the compound. The complex is detected, if present, thereby identifying the MOLX polypeptide within the sample.

20 The invention also includes methods to identify specific cell or tissue types based on their expression of a MOLX.

Also included in the invention is a method of detecting the presence of a MOLX nucleic acid molecule in a sample by contacting the sample with a MOLX nucleic acid probe or primer, and detecting whether the nucleic acid probe or primer bound to a MOLX nucleic
25 acid molecule in the sample.

In a further aspect, the invention provides a method for modulating the activity of a MOLX polypeptide by contacting a cell sample that includes the MOLX polypeptide with a compound that binds to the MOLX polypeptide in an amount sufficient to modulate the activity of said polypeptide. The compound can be, *e.g.*, a small molecule, such as a nucleic
30 acid, peptide, polypeptide, peptidomimetic, carbohydrate, lipid or other organic (carbon-containing) or inorganic molecule, as further described herein.

Also within the scope of the invention is the use of a therapeutic in the manufacture of a medicament for treating or preventing disorders or syndromes including, *e.g.*, endometriosis, fertility disorders, hypercoagulation, idiopathic thrombocytopenic purpura,

immunodeficiencies, systemic lupus erythematosus, asthma, emphysema, scleroderma, allergy, ARDS, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, multiple sclerosis, ulcers, ataxia-telangiectasia, leukodystrophies, behavioral disorders, addiction, anxiety, pain, neuroprotection, osteoporosis, arthritis, ankylosing spondylitis, scoliosis, diabetes, autoimmune disease, myasthenia gravis, muscular dystrophy, renal artery stenosis, interstitial nephritis, glomerulonephritis, polycystic kidney disease, systemic lupus erythematosus, renal tubular acidosis, IgA nephropathy, Lesch-Nyhan syndrome, developmental disorders, growth disorders, and/or wounds, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, obesity, transplantation, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease (GVHD), lymphoedema, adrenoleukodystrophy, congenital adrenal hyperplasia, neuronal developmental, organizational, mediated and interactive disorders and disease; endocrine dysfunctions, growth and reproductive disorders, injury repair, cancer including but not limited to lung or breast cancer, endocrine disorders, inflammatory disorders, gastrointestinal disorders and disorders of the respiratory system, Rheumatoid arthritis (RA), CNS disorders, Down syndrome, Schizophrenia, nutritional deficiencies, primary open-angle glaucoma (POAG), and bone disorders, hematopoietic disorders, or other disorders. The therapeutic can be, *e.g.*, a MOLX nucleic acid, a MOLX polypeptide, or a MOLX-specific antibody, or biologically-active derivatives or fragments thereof.

For example, the compositions of the present invention will have efficacy for treatment of patients suffering from: Cancer including endometriosis, fertility disorders, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, systemic lupus erythematosus, asthma, emphysema, scleroderma, allergy, ARDS, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, multiple sclerosis, ulcers, ataxia-telangiectasia, leukodystrophies, behavioral disorders, addiction, anxiety, pain, neuroprotection, osteoporosis, arthritis, ankylosing spondylitis, scoliosis, diabetes, autoimmune disease, myasthenia gravis, muscular dystrophy, renal artery stenosis, interstitial nephritis, glomerulonephritis, polycystic kidney disease, systemic lupus erythematosus, renal tubular acidosis, IgA nephropathy, Lesch-Nyhan syndrome, developmental disorders, growth disorders, and/or wounds, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial

septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus , pulmonary stenosis , subaortic stenosis, ventricular septal defect (VSD), valve diseases, obesity, transplantation, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease (GVHD), lymphoedema, adrenoleukodystrophy, congenital adrenal hyperplasia, neuronal developmental, organizational, mediated and interactive disorders and disease; endocrine dysfunctions, growth and reproductive disorders, injury repair, cancer including but not limited to lung or breast cancer, endocrine disorders, inflammatory disorders, gastro-intestinal disorders and disorders of the respiratory system, Rheumatoid arthritis (RA), CNS disorders, Down syndrome, Schizophrenia, nutritional deficiencies, primary open-angle glaucoma (POAG), and bone disorders, hematopoietic disorders and/or other pathologies and disorders of the like.

The polypeptides can be used as immunogens to produce antibodies specific for the invention and as vaccines. They can also be used to screen for potential agonist and antagonist compounds. For example, a cDNA encoding MOLX may be useful in gene therapy, and MOLX may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from endometriosis, fertility disorders, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, systemic lupus erythematosus, asthma, emphysema, scleroderma, allergy, ARDS, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, multiple sclerosis, ulcers, ataxia-telangiectasia, leukodystrophies, behavioral disorders, addiction, anxiety, pain, neuroprotection, osteoporosis, arthritis, ankylosing spondylitis, scoliosis, diabetes, autoimmune disease, myasthenia gravis, muscular dystrophy, renal artery stenosis, interstitial nephritis, glomerulonephritis, polycystic kidney disease, systemic lupus erythematosus, renal tubular acidosis, IgA nephropathy, Lesch-Nyhan syndrome, developmental disorders, growth disorders, and/or wounds, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus , pulmonary stenosis , subaortic stenosis, ventricular septal defect (VSD), valve diseases, obesity, transplantation, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease (GVHD), lymphoedema, adrenoleukodystrophy, congenital adrenal hyperplasia, neuronal developmental, organizational, mediated and interactive disorders and disease; endocrine dysfunctions, growth and reproductive disorders, injury repair, cancer including but not limited to lung or breast cancer, endocrine disorders, inflammatory disorders, gastro-

intestinal disorders and disorders of the respiratory system, Rheumatoid arthritis (RA), CNS disorders, Down syndrome, Schizophrenia, nutritional deficiencies, primary open-angle glaucoma (POAG), and bone disorders, hematopoietic disorders and/or other pathologies and disorders.

5 The invention further includes a method for screening for a modulator of disorders or syndromes including, *e.g.*, endometriosis, fertility disorders, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, systemic lupus erythematosus, asthma, emphysema, scleroderma, allergy, ARDS, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, 10 cerebral palsy, epilepsy, multiple sclerosis, ulcers, ataxia-telangiectasia, leukodystrophies, behavioral disorders, addiction, anxiety, pain, neuroprotection, osteoporosis, arthritis, ankylosing spondylitis, scoliosis, diabetes, autoimmune disease, myasthenia gravis, muscular dystrophy, renal artery stenosis, interstitial nephritis, glomerulonephritis, polycystic kidney disease, systemic lupus erythematosus, renal tubular acidosis, IgA nephropathy, Lesch-Nyhan 15 syndrome, developmental disorders, growth disorders, and/or wounds, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, obesity, transplantation, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus 20 host disease (GVHD), lymphoedema, adrenoleukodystrophy, congenital adrenal hyperplasia, neuronal developmental, organizational, mediated and interactive disorders and disease; endocrine dysfunctions, growth and reproductive disorders, injury repair, cancer including but not limited to lung or breast cancer, endocrine disorders, inflammatory disorders, gastro- 25 intestinal disorders and disorders of the respiratory system, Rheumatoid arthritis (RA), CNS disorders, Down syndrome, Schizophrenia, nutritional deficiencies, primary open-angle glaucoma (POAG), and bone disorders, hematopoietic disorders or other disorders related to cell signal processing and metabolic pathway modulation. The method includes contacting a test compound with a MOLX polypeptide and determining if the test compound binds to said MOLX polypeptide. Binding of the test compound to the MOLX polypeptide indicates the 30 test compound is a modulator of activity, or of latency or predisposition to the aforementioned disorders or syndromes.

Also within the scope of the invention is a method for screening for a modulator of activity, or of latency or predisposition to an disorders or syndromes including, *e.g.*, endometriosis, fertility disorders, hypercoagulation, idiopathic thrombocytopenic purpura,

immunodeficiencies, systemic lupus erythematosus, asthma, emphysema, scleroderma, allergy, ARDS, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, multiple sclerosis, ulcers, ataxia-telangiectasia, leukodystrophies, behavioral disorders, addiction, anxiety, pain, neuroprotection, osteoporosis, arthritis, ankylosing spondylitis, scoliosis, diabetes, autoimmune disease, myasthenia gravis, muscular dystrophy, renal artery stenosis, interstitial nephritis, glomerulonephritis, polycystic kidney disease, systemic lupus erythematosus, renal tubular acidosis, IgA nephropathy, Lesch-Nyhan syndrome, developmental disorders, growth disorders, and/or wounds, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, obesity, transplantation, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease (GVHD), lymphoedema, adrenoleukodystrophy, congenital adrenal hyperplasia, neuronal developmental, organizational, mediated and interactive disorders and disease; endocrine dysfunctions, growth and reproductive disorders, injury repair, cancer including but not limited to lung or breast cancer, endocrine disorders, inflammatory disorders, gastrointestinal disorders and disorders of the respiratory system, Rheumatoid arthritis (RA), CNS disorders, Down syndrome, Schizophrenia, nutritional deficiencies, primary open-angle glaucoma (POAG), and bone disorders, hematopoietic disorders or other disorders related to cell signal processing and metabolic pathway modulation by administering a test compound to a test animal at increased risk for the aforementioned disorders or syndromes. The test animal expresses a recombinant polypeptide encoded by a MOLX nucleic acid. Expression or activity of MOLX polypeptide is then measured in the test animal, as is expression or activity of the protein in a control animal which recombinantly-expresses MOLX polypeptide and is not at increased risk for the disorder or syndrome. Next, the expression of MOLX polypeptide in both the test animal and the control animal is compared. A change in the activity of MOLX polypeptide in the test animal relative to the control animal indicates the test compound is a modulator of latency of the disorder or syndrome.

In yet another aspect, the invention includes a method for determining the presence of or predisposition to a disease associated with altered levels of a MOLX polypeptide, a MOLX nucleic acid, or both, in a subject (e.g., a human subject). The method includes measuring the amount of the MOLX polypeptide in a test sample from the subject and comparing the amount of the polypeptide in the test sample to the amount of the MOLX polypeptide present in a

control sample. An alteration in the level of the MOLX polypeptide in the test sample as compared to the control sample indicates the presence of or predisposition to a disease in the subject. Preferably, the predisposition includes, *e.g.*, endometriosis, fertility disorders, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, systemic lupus erythematosus, asthma, emphysema, scleroderma, allergy, ARDS, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, multiple sclerosis, ulcers, ataxia-telangiectasia, leukodystrophies, behavioral disorders, addiction, anxiety, pain, neuroprotection, osteoporosis, arthritis, ankylosing spondylitis, scoliosis, diabetes, autoimmune disease, myasthenia gravis, muscular dystrophy, renal artery stenosis, interstitial nephritis, glomerulonephritis, polycystic kidney disease, systemic lupus erythematosus, renal tubular acidosis, IgA nephropathy, Lesch-Nyhan syndrome, developmental disorders, growth disorders, and/or wounds, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, obesity, transplantation, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease (GVHD), lymphoedema, adrenoleukodystrophy, congenital adrenal hyperplasia, neuronal developmental, organizational, mediated and interactive disorders and disease; endocrine dysfunctions, growth and reproductive disorders, injury repair, cancer including but not limited to lung or breast cancer, endocrine disorders, inflammatory disorders, gastro-intestinal disorders and disorders of the respiratory system, Rheumatoid arthritis (RA), CNS disorders, Down syndrome, Schizophrenia, nutritional deficiencies, primary open-angle glaucoma (POAG); and bone disorders, hematopoietic disorders. Also, the expression levels of the new polypeptides of the invention can be used in a method to screen for various cancers as well as to determine the stage of cancers.

In a further aspect, the invention includes a method of treating or preventing a pathological condition associated with a disorder in a mammal by administering to the subject a MOLX polypeptide, a MOLX nucleic acid, or a MOLX-specific antibody to a subject (*e.g.*, a human subject), in an amount sufficient to alleviate or prevent the pathological condition. In preferred embodiments, the disorder, includes, *e.g.*, endometriosis, fertility disorders, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, systemic lupus erythematosus, asthma, emphysema, scleroderma, allergy, ARDS, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, multiple sclerosis, ulcers, ataxia-telangiectasia,

leukodystrophies, behavioral disorders, addiction, anxiety, pain, neuroprotection, osteoporosis, arthritis, ankylosing spondylitis, scoliosis, diabetes, autoimmune disease, myasthenia gravis, muscular dystrophy, renal artery stenosis, interstitial nephritis, glomerulonephritis, polycystic kidney disease, systemic lupus erythematosus, renal tubular acidosis, IgA nephropathy, Lesch-Nyhan syndrome, developmental disorders, growth disorders, and/or wounds, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, obesity, transplantation, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease (GVHD), lymphoedema, adrenoleukodystrophy, congenital adrenal hyperplasia, neuronal developmental, organizational, mediated and interactive disorders and disease; endocrine dysfunctions, growth and reproductive disorders, injury repair, cancer including but not limited to lung or breast cancer, endocrine disorders, inflammatory disorders, gastro-intestinal disorders and disorders of the respiratory system, Rheumatoid arthritis (RA), CNS disorders, Down syndrome, Schizophrenia, nutritional deficiencies, primary open-angle glaucoma (POAG), and bone disorders, hematopoietic disorders, and/or other diseases or disorders.

In yet another aspect, the invention can be used in a method to identify the cellular receptors and downstream effectors of the invention by any one of a number of techniques commonly employed in the art. These include but are not limited to the two-hybrid system, affinity purification, co-precipitation with antibodies or other specific-interacting molecules.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention is based, in part, upon the discovery of novel nucleic acid sequences that encode novel polypeptides. The novel nucleic acids and their encoded polypeptides are referred to individually as MOL1, MOL2, MOL3, MOL4, MOL5, MOL6, MOL7, and MOL8.

5 The nucleic acids, and their encoded polypeptides, are collectively designated herein as "MOLX".

The novel MOLX nucleic acids of the invention include the nucleic acids whose sequences are provided in Tables 1A, 1D, 2A, 3A, 3D, 4A, 5A, 5C, 5E, 6A, 7A, and 8A. inclusive ("Tables 1A - 8A"), or a fragment, derivative, analog or homolog thereof. The novel
10 MOLX proteins of the invention include the protein fragments whose sequences are provided in Tables 1B, 1E, 2B, 3B, 3E, 4B, 5B, 5D, 5F, 6B, 7B, and 8B inclusive ("Tables 1B - 8B"). The individual MOLX nucleic acids and proteins are described below. Within the scope of this invention is a method of using these nucleic acids and peptides in the treatment or prevention of a disorder related to cell signaling or metabolic pathway modulation.

15 MOL1

MOL1a

A disclosed Notch-like nucleic acid of 7410 nucleotides, MOL1a, alternatively referred to as SC29674552_EXT, is shown in Table 1A. The disclosed MOL1a open reading frame ("ORF") begins at the ATG initiation codon at nucleotides 1-3 and terminates at a TGA codon
20 at nucleotides 7408-7410. In Table 1A, the start and stop codons are depicted with bold letters.

Table 1A. MOL1a nucleotide sequence (SEQ ID NO:1).

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ATGCCCCCGCTGCGCCCGCTCTGCTGTGGGCGCTGCTGGCGCTCTGGCTGTGCTGCGCGACCCCGCGCATGCATT
GCAGTGTGCGAGATGGCTATGAACCGTGTGTAATGAAGGAATGTGTGTTACCTACCACAATGGCACAGGATACTGCA
AATGTCCAGAAGGCTTCTTGGGGGAATATTGTCAACATCGAGACCCCTGTGAGAAGAACCGCTGCCAGAATGGTGGG
ACTTGTGTGGCCAGGCCATGCTGGGGAAAGCCAGTGCCGATGTGCCCTCAGGGTTTACAGGAGAGGACTGCCAGTA
CTCGACATCTCATCCATGCTTTGTGTCTCGACCTTGCCCTGAATGGCGGCACATGCCATATGCTCAGCCGGGATACCT
ATGAGTGCACCTGTCAAGTCGGGTTTACAGGTAAGGAGTGCCAATGGACGGATGCCTGCCTGTCTCATCCCTGTGCA
AATGGAAGTACCTGTACCCTGTGGCCAACAGTTCTCCTGCAAATGCCTCACAGGCTTCACAGGGCAGAAATGTGA
GACTGATGTCAATGAGTGTGACATTCAGGACACTGCCAGCATGGTGGCACCTGCCTCAACCTGCCTGGTTCCTACC
AGTGCCAGTGCCCTCAGGGCTTCACAGGCCAGTACTGTGACAGCCTGTATGTGCCCTGTGCACCCCTCACCTTGTGTC
AATGGAGGCACCTGTGGCAGACTGGTGACTTCACTTTTGAAGTGGCATTACCAGGTTTGAAGGGAGCACCTGTGA
GAGGAATATTGATGACTGCCCTAACCCACAGGTGTGAGAATGGAGGGGTTTGTGTGGATGGGGTCAACACTTACAAC
GCCGCTGTCCCCCAATGGACAGGACAGTTCTGCACAGAGGATGTGGATGAATGCCTGCTGCAGCCCAATGCCTGT
CAAACTGGGGCACCTGTGCCAACCGCAATGGAGGCTATGGCTGTGTATGTGTCAACGGCTGGAGTGGAGATGACTG
CAGTGAGAACATTGATGATTGTGCTTTTGGCGCCTGTACTCCAGGCTCCACCTGCATCGACCGTGTGGCTCCTTCT
CTTGATGTGCCCAGAGGGGAAGGCAGGTCTCCTGTGTCTGATGATGCATGCATCAGCAATCCTTGCCACAAG
GGGGCACTGTGTGACACCAACCCCTAAATGGGCAATATATTGACACCTGCCACAAGGCTACAAAGGGGCTGACTG
CACAGAAGATGTGGATGAATGTGCCATGGCCAATAGCAATCCTTGTGAGCATGCAGGAAAATGTGTGAACACGGATG
GCGCCTTCCACTGTGAGTGTCTGAAGGGTTATGCAGGACCTCGTTGTGAGATGGACATCAATGAGTGCCATTTCAGAC
CCCTGCCAGAATGATGCTACCTGTCTGGATAAGATTGGAGGCTTTCACATGTCTGTGCATGCCAGGTTTCAAAGGTGT
GCATTGTGAATTAGAAATAAATGAATGTGAGAGCAACCTTGTGTGAACAATGGGCAGTGTGTGGATAAAGTCAATC
GTTTCCAGTGCCTGTGTCTCCTGGTTTCACTGGGCCAGTTTGCCAGATTGATATTGATGACTGTTCCAGTACTCCG

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TGCTGAATGGGGCAAAGTGTATCGATCACCCGAATGGCTATGAATGCCAGTGTGCCACAGGTTTCACTGGTGTGTT
GTGTGAGGAGAACATTGACAACGTGTGACCCGATCCTTGCCACCAGTGTGAGTGTGAGGATGGTATTGATTCTTACA
CTTGCATCTGCAATCCCGGTACATGGGCGCCATCTGCAGTGACAGATTGATGAATGTTACAGCAGCCCTTGCCTG
AACGATGGTGCCTGACCTGGTCAATGGCTACCAGTGCAACTGCCAGCCAGGCACGTGAGTGTAAATTGTGA
AATTAATTTTGTGACTGTGCAAGTAACCTTGTATCCATGGAATCTGTATGGATGGCATTAAATCGCTACAGTTGTG
TCTGCTCACCAGGATTCAAGGCGAGATGTAACATTGACATTGATGAGTGTGCTTCCAATCCCTGTGCGAAGGGT
GCAACATGTATCAACGGTGTGAATGGTTTCCGCTGTATATGCCCCGAGGGACCCCATCACCCAGCTGCTACTACA
GGTGAACGAATGCCTGAGCAATCCCTGCATCCATGAAACTGTACTGAGGTTCTCAGTGGATATAAGTGTCTCTGTG
ATGCAGGCTGGGTTGGCATCACTGTGAAGTGGACAAAATGAATGCCTTTCGAATCCATGCCAGAATGGAGGAACT
TGTGACAATCTGGTGAATGGATACAGGTGTACTTGAAGAAGGGCTTTAAAGGCTATAAAGCTGCCAGTGAATATTGA
TGAATGTGCCCTCAAATCCATGCCCTGAACCAAGGAACCTGCTTTGATGACATAAGTGGCTACACTTGGCACTGTGTGC
TGCCATACACAGGTAAGAATTGTGACAGATATTGGCTCCCTGTTCCCAAACCTTGTGAGAATGCTGCTGTTTGC
AAAGAGTCAACAAATTTTGTAGATTATCTTGCTTGTGTGCTTCCGCTGGCTGGCAAGGTGACGGTGTACCATTGACAT
TGACGAGTGTATCTCCAAGCCCTGCATGAACCATGGTCTCTGCCATAACACCAGGGCAGCTACATGTGTGAATGTC
CACCAGGCTTCACTGGTATGGACTGTGAGGAGGACATTGATGACTGCCTTGCAGTCTTCCAGTGAATATTGA
TGTATGGATGGAGTGAATACCTTCTCTGCTGCTTGCCTTCCGCTTCCGCTTCACTGGGGATAAGTGGCAGACAGATGAA
TGAGTGTCTGAGTGAACCTGTAGAATGGAGGGACCTGCTCTGACTACGTCAACAGTTACACTTGCAGTGGCAGG
CAGGATTTGATGGAGTCCATTGTGAGAACAACATCAATGAGTGAAGTGAAGTCTCTGTTTCAATGGTGGCAGATGT
GTTGATGGGATTAACTCCTTCTCTGCTTGTGCTTGTGGGTTTCACTGGATCCTTCTGCTCCATGAGATCAATGA
ATGCAGCTCTCATCATGCTGAATGATGGAACGTGTGTTGATGGCTGGGTACCTACCGCTGCAGTCCGCCCTGG
GCTACACTGGGAAAACTGTGACACCTGGTGAATCTCTGAGTGCCTTGCAGTGGTCTCCATGTAAAAACAAAGGTACTTGGCTT
CAGAAAAAAGCAGAGTCCAGTGCCTATGTCCATCTGGATGGGCTGGTGCCTATTGTGACGTGCCCAATGTCTCTTG
TGACATAGCAGCCTCCAGGAGAGGTGTGCTTGTGAACTTGTGCCAGCACTCAGGTGTCTGCATCAATGCTGGCA
ACACGATTACTGTGAGTCCCTTGGGCTATACTGGAGCTACTGTGAGGAGCAACTCGATGAGTGTGCTTCAAC
CCCTGCCAGCAGGGGCAACATGCAAGTGAATTTGATGGTGAATACAGATGCGAGTGTGCTCAGGCTATCAGGCTGT
CAACTGTGAGTATGAAGTGGATGAGTGCAGAAATCAGCCCTGCCAGAAATGGAGGACCTGTATTGACCTTGTGAACC
ATTTCAAGTGTCTTGGCCACCAGGCACTCGGGGTATGAAATCATCCTTATCCATTTTCAATTGCCCGGGTCCCAT
TGCTTAAATGGTGGTCACTGCATGGATAGGATGGAGGTACAGTGTGCTGCTTGCCTGGCTTGTGCTGGGAGCG
TTGTGAGGGAGACATCAACGAGTGCCTCTCCAACCCCTGCAGCTCTGAGGGCAGCTGGACTGTATACAGCTCACCA
ATGACTACCTGTGTGTTTGGCGTAGTGCCTTTACTGGTGGCACTGTGAAACCTTGTGATGTTGCTCCAGATG
CCCTGCTGAAATGGAGGGACTTGTGCTGTGGCCAGTAACATGCTGATGGTTCATTGTGCTCCAGATG
TTCCGGGGCAAGGTGCCAGAGCAGCTGTGGACAAGTGAATGTAGGAAGGGGAGCAGTGTGTGCACACCCGCTCTG
GACCCGCTGCTTCTGCCCCAGTCCCGGGACTGCGAGTCAAGGCTGTGCCAGTAGCCCTGCCAGCAGGGGGCAGC
TGCCACCTCAGCGCCAGCCTCCTTATTAATCTCTGCCAGTGTGCCCCACCATTTCTCGGGTAGCCGCTGTGAATCTTA
CAGGCAACCCCAAGCAGCCCTCCTGCCACCTGTCTGAGCCAGTATTGTGCCGACAAAGCTCGGGATGGCGTCTGTG
ATGAGGCTGCAACAGCCATGCTGCCAGTGGGATGGGCTGACTGTCTCTCACCATTGGAGAACCCCTGGGCCAAC
TGCTCCTCCCCACTTCCCTGTGCGGATTTATATCAACAACAGTGTGATGAGTGTGCAACAGGTCGAGTGCCTGTT
TGACAACCTTTGAATGCCAGGGGAACAGCAAGACATGCAAGTATGACAAATCTGTGACAGACCTTCAAAGACAACC
ACTGTGACAGGGGTGCAACAGTGAAGTGTGCTTGGGATGGGCTGGACTGTGCTGTGACCAACCTGAGAACCTG
GCAGAAGGTACCTGGTTATTGTGGTATTGATGCCACCTGAACAACCTGCTCCAGGATGCTCGAGCTTCTTGGCGG
ACTGGGTACCTGCTCCACCAACCTGCGCATTAAGACGGGACTCCAGGGGAACTCATGGTGTACCCCTATTATG
TGTGAAAGTCAAGTGTATGAAGAAACAGAGGATGACACGAGATCCCTTCTGCTGTAACAAGAACAGGAGTGGCT
GGGTCTAAAGTCTTCTGGAATTGACAACCGCCAGTGTGTTCAAGACTCAGACCACTGCTTCAAGAACACGGATGC
AGCAGCAGCTCTCCTGGCCTCTCAGCCATACAGGGACCTGTGATACCTCTTGTGTCTGTGCTCAGTGAAGTCCC
TGACTCCAGAACGCACTCAGCTCCTCTATCTCCTTGTGTTGTGCTGTTGTCATCTTCTGTTTATTATTCTGTGGGG
GTAATCATGGCAAAACGAAAGCGTAAGCATGGCTCTCTCTGGCTGCCTGAAGGTTTCACTCTTCCGCGAGATGCAAG
CAATCACAAGCGTCTGTGAGCCAGTGGGACAGGATGCTGTGGGCTGAAAAATCTCTCAGTGAAGTCTCAGAAGCTA
ACCTAATTGGTACTGGAACAAGTGAACACTGGGTCGATGATGAAGGGCCCCAGCCAAAGAAAGTAAAGGCTGAAGAT
GAGGCTTACTCTCAGAAGAAGATGACCCATTGATCGACGGCCATGACACAGCAGCAGCTTGAAGCTGCAGACAT
CCGTAGGACACCATCGCTGGCTCTACCCCTCCTCAGGCAGAGCAGGAGGTGGATGTGTTAGATGTGAATGTCCGTG
GCCAGATGGCTGCACCCCATTTGATGTTGGCTTCTCTCCAGGAGGCAGCTCAGATTGAGTGTGAAGTGAAGAT
GCAGAGGACTCTTCTGCTAACATCATCAGACTTGGTCTACCCAGGCTGCCAGCTCCAGGCCAGACAGACCGGAC
TGGTGAAGATGGCCCTGCACCTTGCAGCCCGCTACTCACGGGCTGATGCTGCCAAGCGTCTCCTGGATGCAGGTGCAG
ATGCCAATGCCAGGACAACATGGGCCGCTGTCCATTCATGCTGAGTGGCAGCTGATGCCAAGGTGTCTTCCAG
ATTTGTGATTCGCAACCGAGTAACCTGATCTAGATGCCAGGATGAATGATGGTACTACACCCCTGATCCTGGCTGCCCG
CCTGGCTGTGGAGGGAATGGTGGCAGAACTGATCAACTGCCAAGCGGATGTGAATGAGTGGATGACCATGGAAAAAT
CTGCTCTTCACTGGGCACTGCTGTCAATAATGTGGAGGCAACTCTTTTGTGTTGAAAAATGGGGCAACCGAGAC
ATGCAGGACAAACAGGAAGAGACACCTCTGTTTCTGTGCTGCCCGGGAGGGAGCTATGAAGCAGCAAGATCCTGTT
AGACCATTTTGGCAATCGAGACATCAGACCATATGGATCGTCTTCCCGGGATGTGGCTCGGGATCGCATGCACC
ATGACATTTGTGCGCCTTCTGGATGAATACATGTGACCCCAAGCCCTCCAGGCACCGTGTGACTTCTGCTCTCTCA
CCTGTCATCTGTGGGCCCAACAGATCTTCTCAGCCTGAAGCACACCCCAATGGGCAAGAGTCTAGACGGCCAG
TGCCAAGAGTACCATGCTTACTAGCCTCCCTAACCTTGCCAAGGAGGCAAGGATGCCAAGGGTAGTAGGAGGAAGA
AGTCTCTGAGTGAAGAGTCCAACCTGTGAGAGTTCAGTAACCTTATCCCTGTTGATTCCCTAGAATCTCCTCAC
ACGTATGTTTCCGACACACATCCTCTCAATGATTACATCCCTGGGATCTTACAGGCCTCACCAACCTTATGTT
GGCCACTGCCCGCCCTCTGCCCCAGTCCATGCCAGCATGCACTATCTTTTCTAACCTTCATGAAATGCAGCCTT
TGGACATGGGGCCAGCACTGTGCTTCCCTCAGTGAGCCAGTTGCTATCCCAACCAACATTTGTGCTCCAGGCAGT
GGCAGTGTGGAAGCTTGTAGTAGGCTCCATCCAGTCCAGTCCAGCAGATTGGATGAACCGCATGGAGGTGAATGA
GACCCAGTACAATGAGATGTTTGGTATGGTCTGGCTCCAGCTGTAGGGCACCCATCCTGGCATAGCTCCCGAGAGA
GGCCACCTGAAGGGAAGCACATAACCAACCCCTCGGGAGCCCTTGGCCCCCATTTGACTTTCAGCTCATCCCTAAA


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GGCAGTATTGCCCAACCAGCGGGGGCTCCCCAGCCTCAGTCCACCTGCCCTCCAGCTGTTGCGGGCCCCCTGCCAC
CATGTACCAGATTCCAGAAATGGCCCCGTTTGCCCACTGTGGCTTTCCCACTGCCATGATGCCCCAGCAGGACGGGC
AGGTAGCTCAGACCATTCTCCAGCCTATCATCTTTCCAGCCTCTGTGGGCAAGTACCCACACCCCTTCACAG
CACAGTTATGCTTCTCTCAATGCTGCTGAGCGAACCCAGTCACAGTGGTCACCTCCAGGGTGAGCATCCCTACCT
GACACCATCCCCAGAGTCTCTGACCAGTGGTCAAGTTATCACCCACTCTGCTTCTGACTGGTCAGATGTGACCA
CCAGCCCTACCCCTGGGGGAGCTGGAGGAGGTGAGCGGGGACCTGGGACACACATGTCTGAGCCACCACACAACAAC
ATGCAGGTTTATGCGTGA

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The disclosed MOL1a nucleotide encodes a protein which has 2469 amino acid residues, referred to as the MOL1a protein. The MOL1a protein was analyzed for signal peptide prediction and cellular localization. SignalP results predict that MOL1a is cleaved between position 25 and 26 (AHA-LQ) of SEQ ID NO:2. Psort and Hydropathy profiles also predict that MOL1a contains a signal peptide and is likely to be localized in the plasma membrane (Certainty=0.4600). A disclosed MOL1a polypeptide sequence is presented in Table 1B using the one-letter amino acid code.

Table 1B. Encoded MOL1a protein sequence (SEQ ID NO:2).

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MPALRPALLWALLALWLCCATPAHALQCRDGYEPCVNEGMCVITYHNGTGYCKCPEGFLGEYCQHRDPCEKNRCQNGG
TCVAQAMLGKATCRCASGFTGEDCQYSTSHPCFVSRPCLNNGGTCHMLSRDTECTCQVGTGKECQWTDACLSPHPCA
NGSTCTTVANQFSCKCLTGFTGQKCEDVNECDIPGHCHGGTCLNLPGSYQCCPQGTGQYCDLSLYVPCAPSPCV
NGGTCTGTGDFTFECHLPFEGSTCERNIDDCPNHRCQNGGVCVDGVNTYNCRCPPQWTGQFCTEDVDECLLPNAC
QNWGTANRNGGYGCVCVNWSGDDCSENIDDCAFGACTPGSTCIDRVASFSCMCPEGKAGLLCHLDDACISNPCHK
GALCDTNPLNGQYICTCPQGYKGADCTEDVDECAMANSNPCEHAGKCVNTDGAFFHCECLKGAYAGPRCEMDINECHSD
PCQNDATCLDKTGGFTCLCMPGFKGVHCELEINECQSNPCVNNQGVCKVNRFOQLCPGFTGPFVQCIDIDDCSSTP
CLNGAKCIDHPNGYECQCATGFTGVLCKENIDNCDPDPCHHGQCCQDGIDSYTCICNPGYMGAIQSDQIDECYSSPCL
NDGRCIDLVNGYQCNCQPGTSGVNCEINFDDCASNPCHIGICMDGINRYSCVCSPGFTGQRCNIDIDECASNPCRKG
ATCINGVNGFRICIPEGPHHPSCYSQVNECLSNPCHIGNCTGGLSGYKCLCDAGWVGINCEVDKNECLSNPCQNGGT
CDNLVNGYRCTCKKGFKNQVNIIDECASNPCLNQGTCPDDISGYTCHCVLPYTGNKQTVLAPCSPNPNCEAANC
KESPNFESYTCCLCAPGWQGRCTIDIDECISKPMNHGLCHNTQGSYMCCEPPGFSGMDCEEDIDDCLASPCQNGGS
CMDGVNTFSCCLCPGFTGDKCQTDMECLSEPCNNGGTCSYVNSYTKCQAGFDGVHCENNINECTESSCFNGGTC
VDGINSFSCCLCPVGTGTSFCLHEINECSSHPCLNDGTCDGLGTYRCSCPLGYTGKNCQTLVNLCSRSPCKNKGTVCV
QKKAESQCLCPSGWAGAYCDVNVSCDIAASRRGVLEHLQCHSGVCINAGNTHYCCPLGYTGSYCEEQLDECBASN
PCQHGATCSDFIGGYRCEVPGYQGVNCEYEVDCEQNPQNGGTCLDLVNHFKCSCPPGTRGMKSSLSIFHCPGPH
CLNGGQCMDRIGYSCRCLPGFAGERCEGDINECLSNPCSSSEGLDCIQLTNDYLCVCRSAFTGRHCETFDVDCPQM
PCLNNGGTCAVASNMPDGSFAVVPQGFSGARCQSSCGQVCKRKEQCQVHTASGPRCFCPSPRDCESGCASSPCQHGGS
CHPQRPYYSCQCAPFSGSRCELYTAPPSTPATCLSQYCADKARDGVCEACNSHACQWDGDCSLTMENPWAN
CSSPLPCWDYINNQCDELNTVECLFDNFCEQGNSTCKYDKYCADHFKDNHCDQGCNSEECCWGDGLDCAADQFENL
AEGTLVIVVLMPEQLQDARSFLRALGTLTLLHTNLRIKDSQGELMVYPYGEKSAAMKKQRMTRSLPGEQBEQVA
GSKVFLIDNRQCVQDSDFKNTDAAAALLASHAIQGTLSYPLVSVVSESLTPERTQLLYLLAVAVVILFIILLG
VIMAKRKRKHGSLWLPEGFTLRRDASNHRKREPVGQDAVGLKNLSVQVSEANLIGTGTSEHWVDDREGPQPKVKAED
EALLSEEDDPIDRRPWTQQLHLEADIRRTPSLALTPQAEQEVVDVLDVNVVRGPDGCTPLMLASLRGGSSDLSEDED
AEDSSANIITDLVYQGASLQAQTDRTGEMALHLAARYSRADAARLLDAGADANAQDNMGRCPHLHAAVAADAQGVFQ
ILIRNRVTDLDARMNDGTTPLILAAARLAVEGMVAELINCQADVNAVDDHGKSALHWAANVNVEATLLLLKNGANRD
MQDNKEETPLFLAAREGSYEAALILDDHFANRDI TDHMDRLPRDVARDRMHHDIVRLLEYNVTSPSPGTVLTSALS
PVICGPNRSFLSLKHTPMGKSRPSAKSTMPTSLPNLAKEAKDAKGSRRKSLSEKVLSESSVTLSPVDSLESPI
TYVSDTTSSPMITSPGILQASPNPMLATAAPPAPVHAQHLSFSLNHEMQPLAAGASTVLPSVSQLSHHHIVSPGS
GSAGSLRSLHPVVPADWMNRMEVNETQYNEMFGMVLAPAVGHPSWHSSPERPPEGKHIITPREPLPIVTFQLIPK
GSIAQPAQAPQPOSTCPPAVAGPLPTMYQIPEMARLPSVAFPTAMMPQDQVQATILPAYHPPASVGKYPTPPSQ
HSYASSNAERTPSHSHLQGEHPYLTSPSPESPDQWSSSPHSASDWSVDTTSPTPGGAGGGQRPCTHMEPPHNN
MQVYA

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A region of the MOL1a nucleic acid sequence has 6436 of 7416 bases (86%) identical to a *Rattus norvegicus* Notch-like protein mRNA (GENBANK-ID:RATNOTCHX | acc:M93661), with an E-value of 0.0. In all BLAST alignments herein, the "E-value" or

“Expect” value is a numeric indication of the probability that the aligned sequences could have achieved their similarity to the BLAST query sequence by chance alone, within the database that was searched. For example, the probability that the subject (“Sbjct”) retrieved from the MOL1a BLAST analysis, *e.g.*, the *Rattus norvegicus* Notch-like protein mRNA, matched the Query MOL1a sequence purely by chance is 0.0. MOL1a also has 2443 of 2471 amino acid residues (98%) positive with patp:AAY06816 Human Notch2 (humN2) protein sequence - *Homo sapiens*, 2471 aa.

The Expect value is used as a convenient way to create a significance threshold for reporting results. The default value used for blasting is typically set to 0.0001. In BLAST 2.0, the Expect value is also used instead of the P value (probability) to report the significance of matches. For example, an E value of one assigned to a hit can be interpreted as meaning that in a database of the current size one might expect to see one match with a similar score simply by chance. An E value of zero means that one would not expect to see any matches with a similar score simply by chance. See, *e.g.*, <http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/>. Occasionally, a string of X’s or N’s will result from a BLAST search. This is a result of automatic filtering of the query for low-complexity sequence that is performed to prevent artifactual hits. The filter substitutes any low-complexity sequence that it finds with the letter “N” in nucleotide sequence (*e.g.*, “NNNNNNNNNNNNNN”) or the letter “X” in protein sequences (*e.g.*, “XXXXXXXXXX”). Low-complexity regions can result in high scores that reflect compositional bias rather than significant position-by-position alignment. Wootton and Federhen, Methods Enzymol 266:554-571, 1996.

Utilities for the MOLX nucleic acids and their encoded polypeptides can be inferred based on the homology of the disclosed MOLX nucleic acids and/or polypeptides (including domains of the encoded polypeptides) to previously described sequences.

MOL1a expression in different tissues was examined through TaqMan as described below in Example 1.

MOL1a is expressed in at least the following tissues: kidney, brain, lymph node, muscle, hippocampus, bone marrow, placenta, thyroid, para-thyroid, prostate, testis, epidermis, ovary, coronary artery, liver, lung, spinal cord, stomach, breast, lung, uterus, and colon. It is likely that Notch proteins are expressed in all tissues, so the widespread expression of MOL1a agrees with its homology with Notch.

One or more consensus positions (Cons. Pos.) of the nucleotide sequence of MOL1a have been identified as single nucleotide polymorphisms (SNPs) as shown in Table 1C. A

dash ("-"), when shown, means that a base is not present. The sign ">" means "is changed to". SNPs were identified using the techniques disclosed in Example 3.

Table 1C: SNPs for MOL1a			
Consensus Position	Base Change	AA change Position	Residue Change
4288	G > A	1429	A > T
5858	T > C	1952	L > P
5833	A > G	1944	T > A
5366	C > T	1788	T > I

MOL1b

5 MOL1a was subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on *in silico* predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences sequences from other species. These primers were then employed in PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain - whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus. Usually the resulting amplicons were gel purified, cloned and sequenced to high redundancy. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported below, which is designated MOL1b, or alternatively Accession Number CG56250-02. This differs from the previously identified sequence in lacking 996 internal amino acids in addition to a few minor changes.

A disclosed Notch-like nucleic acid of 6728 nucleotides, MOL1b, is shown in Table 1C. The disclosed MOL1b open reading frame ("ORF") begins at the ATG initiation codon at nucleotides 13-15, and terminates at a TGA codon at nucleotides 4431-4434. In Table 1D the start and stop codons are in bold letters, and the untranslated regions are underlined.

5

Table 1D. MOL1b nucleotide sequence (SEQ ID NO:3).

TCATCTGGAATTATGCCCGCCCTGCGCCCCGCTCTGCTGTGGGCGCTGCTGGCGCTCTGGCTGTGCTGCGCGGCCCC
CGCGCATGCATTCAGTGTGAGATGGCTATGAACCTGTGTAAATGAAGGAATGTGTGTACCTACCACAATGGCA
CAGGATACTGCAAATGTCCAGAAGGCTTCTGGGGGAATATTGTCAACATCGAGACCCCTGTGAGAAGAACCCTGTC
CAGAATGGTGGGACTTGTGTGGCCAGGCCATGCTGGGGAAAGCCACGTGCCGATGTGCCTCAGGGTTTACAGGAGA
GGACTGCCAGTACTCAACATCTCATCCATGCTTTGTGTCTCGACCCCTGCCTGAATGGCGGCACATGCCATATGCTCA
GCCGGGATACCTATGAGTGCACCTGTCAAGTCGGGTTTACAGGTAAGGAGTGCCAAATGGACGGATGCCTGCCTGTCT
CATCCCTGTGCAAATGGAAGTACCTGTACCCTGTGGCAACCAAGTTCTCTGCAAATGCCTCACAGGCTTCACAGG
GCAGAAATGTGAGACTGATGTCAATGAGTGTGACATTCCAGGACACTGCCAGCATGGTGGCACCTGCCTCAACCTGC
CTGGTTCTTACCAGTGCAGTGCCTCAGGGCTTCACAGGCCAGTACTGTGACAGCCTGTATGTGCCCTGTGCACCC
TCACCTTGTGTCAATGGAGGCACCTGTGCGGAGACTGGTGACTTCACTTTTGAAGTGAACCTGCCTTCAGGTTTGA
AGGGAGCACCTGTGAGAGGAATATTGATGACTGCCCTAACACAGGTGTGAGAATGGAGGGGTTTGTGTGGATGGGG
TCAACACTTACAACCTGCCGCTGTCCCCACAATGGACAGGACAGTTCTGTCACAGAGGATGTGGATGAATGCCCTGCTG
CAGCCCAATGCCCTGTCAAATGGGGGCACCTGTGCCAACCGCAATGGAGGCTATGGCTGTGTATGTGTCAACGGCTG
GAGTGGAGATGACTGCAGTGAACATTGATGATTGTGCCTTCGCTCCTGTACTCCAGGCTCCACCTGCATCGACC
GTGTGGCCTCCTTCTCTTGCATGTGCCAGAGGGGAAGGCAGGTCTCCTGTGTCTGATGTGATGCATGCATCAGC
AATCCTTGGCACAAGGGGGCACTGTGTGACACCAACCCCTAAATGGGCAATATATTGACCTGCCACAAGGCTA
CAAAGGGGCTGACTGCACAGAAGATGTGGATGAATGTGCCATGGCCAATAGCAATCCTTGTGAGCATGCAGGAAAT
GTGTGAACACGGATGGCGCCTTCCACTGTGAGTGTCTGAAGGGTTATGCAGGACCTCGTTGTGAGATGGACATCAAT
GAGTGCATTTCAGACCCCTGCCAGAATGATGCTACCTGTCTGGATAAGATTGGAGGCTTCACATGTCTGTGCATGCC
AGGTTTCAAAGGTGTGCATTGTGAATTAGAAATAAATGAATGTGAGCAACCCCTTGTGTGAACATGGGCAGTGTG
TGGATAAAGTCAATCGTTTCCAGTGCCCTGTGTCTCCTGGTTTCACTGGGCCAGTTTGGCAGATTGATATTGATGAC
TGTTCCAGTACTCCGTGTCTGAATGGGGCAAAGTGTATCGATCACCAGAATGGCTATGAATGCCAGTGTGCCACAGG
TTTCACTGGTGTGTGTGTGAGGAGAACATTGACAACCTGTGACCCCGATCCTTGCACCATGGTCACTGTGTGAGGATG
TTTGTGATTCTTACACCTGCATCTGCAATCCCGGTACATGGGGCCCATCTGCAGTGACCAGATTGATGAATGTTAC
AGCAGCCCTTGCCTGAACGATGGTGCCTGCATTGACCTGGTCAATGGCTACCAAGTGCAACTGCCAGCCAGGCACGTC
AGGGGTAAATTGTGAAATTAATTTTGTGACTGTGCAAGTAACCCCTGTATCCATGGAATCTGTATGGATGGCATT
ATCGCTACAGTTGTGTCTGCTCACCAGGATTCACAGGGCAGAGATGTAACATTGACATTGATGAGTGTGCCTCCAAT
CCCTGTGCAAGGGTGCAACATGTATCAACGGTGTGAATGGTTTCCGCTGTATATGCCCGAGGGACCCCATCACCC
CAGCTGCTACTCAGAGTGAAACGAATGCCTGAGCAATCCCTGCATCCATGGAACTGTACTGGAGGTCTCAGTGGAT
ATAAGTGTCTCTGTGATGCAGGCTGGGTGGCATCACTGTGAAGTGGACAAAATGAATGCCTTTGCAATCCATGC
CAGAATGGAGGAACCTGTGACAATCTGGTGAATGGATACAGGTGTACTTGAAGAAGGGCTTTAAAGGCTATAACTG
CCAGGTGAATATTGATGAATGTGCCTCAAATCCATGCCTGAACCAAGGAACCTGCTTTGATGACATAAGTGGCTACA
CTTGCCACTGTGTGCTGCCATACAGGCAAGAATTGTGACAGAGTATGGCTCCCTGTTCCCAAACCCCTTGTGAG
AATGCTGCTGTTTGAAGAAGTCAACCAATTTTGAAGTTTATACTTGTCTGTGTGCTCCTGGCTGGCAAGGTGAGCG
GTGTACCATTTGACATTGACGAGTGTATCTCAAGCCCTGCATGAACCATGGTCTCTGCCATAACCCAGGGCAGCT
ACATGTGTGAATGTCCACAGGCTTCAGTGGTATGGACTGTGAGGAGGACATTGATGACTGCCTTGCCAATCCTTGC
CAGAATGGAGGTTCTTGTATGGATGGAGTGAATACTTTCTCCTGCCTCTGCCTTCCGGGTTTCACTGGGGATAAGTG
CCAGACAGACATGAATGAGTGTCTGAGTGAACCTGTGAAGATGGAGGACCTGCTCTGACTACGTCAACAGTTACA
CTTGCAAGTGCAGGCAGGATTGATGGAGTCCATTGTGAGAACAAACATCAATGAGTGCATGAGAGTCTCCTGTTT
AATGGTGGCACATGTGTTGATGGGATTAACCTCTCTCTTGTGCTGTGCTGTGGCTTCACTGGATCCTTCTGCCT
CCATGAGATCAATGAATGCAGCTCTCATCCATGCCTGAATGAGGGAACGTGTGTGATGGCTGGGTACCTACCGCT
GCAGCTGCCCCCTGGGCTACACTGGGAAAACTGTGAGACCTGGTGAATCTCTGCAGTCGCTCTCATGTAAAAAC
AAAGGTACTTGTGTTTCAAAAAAGCAGAGTCCCAGTGCCTATGTCCATCTGGATGGGCTGGTGCCTATTGTGACGT
GCCCAATGTCTCTTGTGACATAGCAGCCTCCAGGAGAGGTGTGCTTGTGTAACACTTGTGCCAGCACTCAGGTGCT
GCATCAATGCTGGCAACACGCATTACTGTGAGTGCCTTGGGCTATACTGGGAGCTACTGTGAGGAGCAACTCGAT
GAGTGTGCGTCAACCCCTGCCAGCACGGGGCAACATGCAGTGAATTCATTGGTGGATACAGATGCGAGTGTGTCCC
AGGCTATCAGGGTGTCAACTGTGAGTATGAAGTGGATGAGTGCCAGAATCAGCCCTGCCAGAATGGAGGCACCTGTA
TTGACCTTGTGAACCAATTTCAAGTGTCTTGGCCACCAGGCACTCGGGGCTACTCTGTGAAGAGAACATTGATGAC
TGTGCCCGGGTCCCCATTGCTTAATGGTGGTCAGTGATGGATAGGATTGGAGGCTACAGTTGTCTGCTGCTTGCCT
TGGCTTGTCTGGGGAGCGTTGTGAGGGAGACATCAACGAGTGCCTCTCCAACCCCTGCAGCTCTGAGGGCAGCCTGG
ACTGTATACAGCTCAACATGACTACCTGTGTGTTTGGCTAGTGCCTTTACTGGCCGGCACTGTGAAACCTTCTGTC
GATGTGTGTCCCAGATGCCCTGCCTGAATGGAGGCACTTGTGCTGTGCCCAGTAACATGCCCTGATGGTTTCATTG
CCGTTGTCCCCGGGATTTTCCGGGGCAAGGTACCAGATTCCAGAAATGGCCGTTTGGCCAGTGTGGCTTCCCCA
CTGCCATGATGCCCCAGCAGGACGGGCAGGTAGCTCAGACCAATCTCCAGCCTATCATCCTTCCAGCCTCTGTG
GGCAAGTACCCCAACCCCTTCAAGCAGTATGCTTCTCAAATGCTGTGAGCGAACACCCAGTCAAGTGG
TCACCTCCAGGGTGAAGCATCCCTACCTGACACCATCCCAAGTCTCCTGACCAAGTGGTCAAGTTTCATCCCCCACT
CTGCTTCTGACTGGTGCAGATGTGACCACAGCCCTACCCCTGGGGGTGCTGGAGGAGGTGAGCGGGGACCTGGGACA

CACATGTCCTGAGCCACCACACAACATGCAGGTTTATGCGTGAGAGAGTCCACCTCCAGTGTAGAGACATAACTG
 ACTTTTGTAAATGCTGCTGAGGAACAAATGAAGGTCATCCGGGAGAGAAATGAAGAAATCTCTGGAGCCAGCTTCTA
 GAGGTAGGAAGAGAAGATGTTCTTATTTCAGATAATGCAAGAGAAGCAATTCGTCAGTTTCTAGGGTATCTGCAAG
 GCTTATTGATTATTCTTAATCTAATAAGACAAGTTTGTGGAAATGCAAGATGAATACAAGCCTTGGGTCCATGTTTAC
 TCTCTTCTATTGGAGAATAAGATGGATGCTTATTGAAGCCAGACATTCTTGACGCTTGGACTGCATTTTAAAGCCC
 TGCAGGCTTCTGCCATATCCATGAGAAGATTCTACACTAGCGTCTGTTGGGAATTATGCCCTGGAATTCTGCCTGA
 ATTGACCTACGCATCTCCTCCTCTGGACATCTTTTGTCTTCAATTGGTGTCTTTGGTTTTCACCTCTCCGTGA
 TTGTAGCCCTACCAGCATGTTATAGGGCAAGACCTTTGTGCTTTTGATCATTCTGGCCCATGAAAGCAACTTTGGTC
 TCCTTTCCCTCCTGTCTTCCCGGTATCCCTTGGAGTCTCACAAGGTTTACTTTGGTATGGTCTCAGCACAAACCT
 TTCAAGTATGTTGTTTCTTTGGAAAATGGACATACTGTATTGTGTTCTCCTGCATATATCATTTCTGGAGAGAGAAG
 GGGAGAAGAATACTTTTCTTCAACAATTTTGGGGGAGGAGATCCCTTCAAGAGGCTGCACCTTAATTTTCTGTG
 CTGTGTGACAGTCTTCATATAAACTTTACCAGGAAGAAGGGTGTGAGTTTGTGTTTTTCTGTGTATGGGCTGGTC
 AGTGTAAAGTTTATCCTTGATAGTCTAGTTACTATGACCTCCCACTTTTTTAAACCAGAAAAGGTTTGGAAAT
 GTTGAATGACCAAGAGACAAGTTAACTCGTGCAAGAGCCAGTTACCCACCCACAGGTCCCCCTACTTCTGCCAAG
 CATTCATTGACTGCCTGTATGGAACACATTTGTCCGATCTGAGCATTCTAGGCCTGTTTCACTCACTACCCAG
 CATATGAACTAGTCTTAACTGTTGAGCCTTTCTTTTATATCCACAGAAGACACTGTCTCAAATGTTGTACCCCTG
 CCATTAGGACTGAACCTTTCTTAGCCCAAGGAGCCAGTGACAGTTGTCTTCCGTTTGTGATGATCAGTCTCTA
 CTGATTATCTTCTGCTTAAAGGCCTGCTCACCATCTTTCTTTTCAACCGTGTGGTCCGTGTTACTGGTATACCCA
 GTATGTTCTCACTGAAGACATGGACTTTATATGTTCAAGTGCAGGAATTGGAAGTTGGACTGTTTCTATGATCC
 AAAACAGCCCTATAAGAAGGTTGGAAGGAGGAATATATAGCAGCCTTTGCTATTTTCTGTACCATTTCTTTTC
 CTCTGAAGCGGCATGACATTTCCCTTTGGCACTAACGTAGAAAATCAACAGAACATTTCTTCTTAGAGTCAAC
 TTTTAGATGATAATGGACAATATAGACTTGCTCATTGTTGAGACTGATTGCCCTCACCTGAATCCACTCTCTGTA
 TTCATGCTCTTGGCAATTTCTTGAATTTCTTTTAAAGGAGAGAAGCATTTAGTTAATTGTAGATAAAGAATAGTTT
 TCTTCTCTTCTCCTTGGGCCAGTTAATAATTGGTCCATGGCTACACTGCAACTTCCGTCAGTGCTGTGATGCCA
 TGACACCTGCAAAATAAGTTCTGCCCTGGGCATTTGTAGATATTAAAGGTTAATCCGACTCTTTTGGTTTGAAT
 GACAGTTCTCATTTCTTCTATGGCTGCAAGTATGCATCAGTGCTTCCCACTTACCTGATTTGTCTGTGCGGTGGCCCC
 ATATGGAACCCCTGCGTGTCTGTTGGCATAATAGTTTACAAATGGTTTTTTTCAGTCTATCCAAATTTATTGAACCA
 ACAAAATAATTACTTCTGCCCTGAGATAAGCAGATTAAAGTTTGTTCATTCTCTGCTTTATTCTCTCCATGTGGCA
 CATTCTGTGAGCTCTTTTATAGTGTGCAACATTTTATCATTCTAAATGGTACTCTCTGCCCTTGGACCCATTTA
 TTATTACAGATGGGGAGAACCTATCTGCATGGACCCTCACCATCTCTGTGACGACACACAGTGCAGGGAGCCAG
 TGGCGATGGCGATGACTTTCTTCCCCTGG

The protein encoded by the MOL1b nucleic acid sequence has 2469 amino acid residues, and is disclosed in Table 1E. The MOL1b protein was analyzed for signal peptide prediction and cellular localization. SignalP results predict that MOL1b is cleaved between position 25 and 26 (AHA-LQ) of SEQ ID NO:4. Psort and Hydropathy profiles also predict that MOL1b contains a signal peptide and is likely to be localized extracellularly (Certainty=0.7666).

Table 1E. Encoded MOL1b protein sequence (SEQ ID NO:4).

MPALRPALLWALLALWLCCAAPAHALQCRDGYEPCVNEGMCVITYHNGTGYCKCPEGFLGEYCQHRDPCEKNRCQNGG
 TCVAQAMLGKATCRCASGFTGEDCQYSTSHPCFVSRPLNGGTCHMLSRDYEECTCQVGFTGKECQWTDACLSPCA
 NGSTCTTVANQFSCKCLTGFTGQKCE TDVNECDIPGHCHGGTCLNLPGSYQCQCPQGFTGQYCDLSLVPCAPSPCV
 NGGTCRQTGDFTECNCLPGFEGSTCBRNIDDCPNHRCQNGGVCVDGVNTYNCRCPPQWTGQFCTEDVDECLLPNA
 CQNGGT CANRNGGYGCVVNGWSGDDCSENIDDAFASCTPGSTCIDRVASFSCMCPEGKAGLLCHLDDACISNPCH
 KGALCDTNPLNGQYICTCPQGYKGADCTEDVDECAMANSNPCEHAGKCVNTDGAHFCECLKGYAGPRCEMDINECHS
 DPCQNDATCLDKIGGFTCLCMPGFGVHCELEINECQSNPCVNNQCVDKVNRFQCLCPGFTGPVCQIDIDDCSST
 PCLNGAKCIDHENGECQCATGFTGVLCEENIDNCDPDPCHHGQDQDIDSYTICINPGYMGAI CSQIDECYSSPC
 LNDGRCIDLVNGYQCNCQPGTSGVNCEINFDDCASNPCHIGICMDGINRYSVCSPGFTGQRCNIDIDECASNPCRK
 GATCINGVNGFRICIPEGPHHPSCYSQVNECLSNPCIHNGCTGGLSGYKCLDAGWVGINCEVDKNECLSNPCQNGG
 TCDNLVNGYRCTCKKGFGYNCQVNIDECASNPCLNQGTCFDDISGYTCHCVLPYTGKNCQTVLAPCSPNPNCEAAV
 CKESPNFESYTCLCAPGWQQRCTIDIDECISKPCMNHGLCHNTQGSYMCECPPGFSGMDCCEEDIDCLANPCQNGG
 SCMDGVNTFSCCLCPGFTGDKCQIDMNECLSEPCKNNGTCSQDYVNSYTCCKQAGFDGVHCENININECTESSCFNGGT
 CVDGINSFSLCPVGFTGSFCLHEINECSSHPCLNEGTCVDGLGTYRCSCLGYTGKNCQTLVNLCRSRSPCKNKGTC
 VQKKAESQCLCPSGWAGAYCDVPNVSCDIAASRRGLVLEHLQHSQVCINAGNTHYQCPLGYTGSYCEEQLDECAS
 NPQHGATCSDFIGGYRCBVPGYQVNCYEVEDECQNPQNGGTCIDLNVHFKCSCPPGTRGLLCEENIDDCARG
 PHCLNGGQCMRIGGYSRCLPGFAGERCEGDINECLSNPCSSSEGLDCIQLTNDYLCVCRSAFTGRHCETFDVDCP
 QMPCILNGGTCVAVSNMDFICRCPGFGSGARYQIPEMARLPSVAFPTAMMPQDQVAQTILPAYHFFPASVGKYP
 TTPSQHSYASSNAERTPSHSGHLQGHYPYLTSPSPDQWSSSSPHSASDWSVDVTTSPTPGGAGGGQGRPGTHMSE

PPHNNMQVYA

A region of the MOL1b nucleic acid sequence, localized to chromosome 1, has 4041 of 4042 bases (99%) identical to a gb:GENBANK-ID:AF308601|acc:AF308601.1 mRNA from Homo sapiens (Homo sapiens NOTCH 2 (N2) mRNA, complete cds), with an E-value of 0.0.

5 The amino acid sequence of MOL1b has 1340 of 1343 amino acid residues (99%) identical to, and 1340 of 1343 amino acid residues (99%) similar to, the 2471 amino acid residue ptr:TREMBLNEW-ACC:AAG37073 protein from Homo sapiens (Human) (NOTCH2 PROTEIN).

10 MOL1b expressed in at least the following tissues: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus, Aorta, Ascending Colon, Bone, Cartilage, Cochlea, Colon, Coronary Artery, Epidermis, Foreskin, Liver, Lung, 15 Lymph node, Lymphoid tissue, Muscle, Nasoepithelium, Ovary, Parathyroid Gland, Parotid Salivary glands, Peripheral Blood, Respiratory Bronchiole, Retina, Synovium/Synovial membrane, Thymus, Tonsils, Umbilical Vein, Vein, Whole Organism.

One or more consensus positions (Cons. Pos.) of the nucleotide sequence of MOL1b have been identified as single nucleotide polymorphisms (SNPs) as shown in Table 1F.

20 "Depth" represents the number of clones covering the region of the SNP. The Putative Allele Frequency (PAF) is the fraction of all the clones containing the SNP. A dash ("-"), when shown, means that a base is not present. The sign ">" means "is changed to".

Table 1F: SNPs for MOL1b			
Consensus Position	Depth	Base Change	PAF
100	24	T > C	0.083
204	23	G > A	0.087
369	23	G > A	0.087

25 The amino acid sequence of MOL1a also had high homology to other proteins as shown in table 1G.

Table 1G. BLAST results for MOL1a					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
<u>gi 104252 pir A35844</u>	Notch protein - African clawed frog	2524	1323/2515 (52%)	1676/2515 (66%),	0.0
<u>>gi 6679096 ref NP_032742.1</u>	Notch gene homolog 3, (Drosophila) [Mus musculus]	2318	665/1515 (43%)	860/1515 (55%)	0.0
<u>gi 13242247 ref NP_077334.1</u>	Notch gene homolog 2, (Drosophila) [Rattus norvegicus]	2471	2251/2472 (91%)	2340/2472 (94%)	0.0
<u>gi 2209059 dbj BA A20535.1</u>	Notch 2 [Takifugu rubripes]	2447	1240/2203 (56%)	1546/2203 (69%)	0.0
<u>gi 6093542 sp Q07008 NTC1_RAT</u>	NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR	2531	1340/2538 (52%)	1683/2538 (65%)	0.0

A ClustalW analysis comparing disclosed proteins of the invention with related OR protein sequences is given in Table 1H, with MOL1a shown on line 1 and MOL1b on line 2.

In the ClustalW alignment of the MOL1a and MOL1b proteins, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (*i.e.*, regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be mutated to a much broader extent without altering protein structure or function. Residue differences between any MOLX variant sequences herein are written to show the residue in the "a" variant and the residue position with respect to the "a" variant. MOL residues in all following sequence alignments that differ between the individual MOL variants are highlighted with a box and marked with the (o) symbol above the variant residue in all alignments herein.

Table 1H. ClustalW Analysis of MOL1a

- 1) Novel MOL1a (SEQ ID NO:2)
- 2) Novel MOL1b (SEQ ID NO:4)
- 3) gi|104252|pir|A35844 Xotch protein - African clawed frog (SEQ ID NO:25)
- 4) gi|6679096|ref|NP_032742.1| Notch gene homolog 3, (Drosophila) [Mus musculus] (SEQ ID NO:26)
- 5) gi|13242247|ref|NP_077334.1| Notch gene homolog 2, (Drosophila) [Rattus norvegicus] (SEQ ID NO:27)
- 6) gi|2209059|dbj|BAA20535.1| Notch 2 [Takifugu rubripes] (SEQ ID NO:28)
- 7) gi|6093542|sp|Q07008|NTC1_RAT NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (SEQ ID NO:29)

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40

5	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> MPALRPALLWALLALWLCCATPAHALCCRDGYEPCVNEGM MPALRPALLWALLALWLCCAAPAHALCCRDGYEPCVNEGM MDRTG---LAVLLCS--LPVLTQGLRPQTQAEMLNGGR -----MGLGARGRRRR-----R-LM MPALRPAAERALLWLWLCCGAGPAHALCCRGGOEPCVNEGT ----- MPRT---LAPLLCLTLFPALARGLRCSQPSGTCVNGGR </pre>
10		50 60 70 80
15	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> CVTYHNGTGYCKRCEGFLGEYCOHRDPC-EKNRCQNGGTC CVTYHNGTGYCKRCEGFLGEYCOHRDPC-EKNRCQNGGTC CEMTFGGTGVCLCGNLTEGERCOFFNPCTIKNOCMNEGTC ALPPPPPPMRALPLLLLPAAGLGAAPPCLDGSPOANGGRC CVTYHNGTGYCKRCEGFLGEYCOHRDPC-EKNRCQNGGTC -----CAPGFLGEYCOHRDPC-QPGYCLNGGNC CEVANG-TEACVCSGARVQCRCQDPSPC-LSTPCKNAGTC </pre>
20		90 100 110 120
25	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> VAQA---MLGKATCRCAAGFTGEDCOYSTSHPCFVSRP VAQA---MLGKATCRCAAGFTGEDCOYSTSHPCFVSRP EPVLQG---NAIDFICHCPVEFTDKVCLTPVDNACVNP-P THQQ-----PSLEAACLCPLGWVERCQL--EDPCHSG-P VTQA---MLGKATCRCAAGFTGEDCOYSTSHPCFVSRP SVSMSAGVPVPGSATCSPLGYAGRCQIPQNSTCYPANE YVVDHG---GIVDYACSPLGFSGPLCLTPLANACLAN-P </pre>
30		130 140 150 160
35	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> CLNGGTCH--MLS-RDTVECTCQVSTGKECQWIDACLSE CLNGGTCH--MLS-RDTVECTCQVSTGKECQWIDACLSE CRNGGTCE--LNSVTEMKCRCPPEWIEDSCQADPCASN CAGRGVQSSVAGTARTSICRLRCGCPDCSQPDPCVSR CONGGTCH--MLS-WDTVECTCQVSTGKECQWIDVCLSE CANRGICT--LTP-FDKVACECARGWTGPGCYELSCISS CRNGGTCD--LIT-LTEVKCRCPPEWIEDSCQADPCASN </pre>
40		170 180 190 200
45	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> PCANGSTCTTVAN-QFSCKLTGFTGCKCETDVNECD-IP PCANGSTCTTVAN-QFSCKLTGFTGCKCETDVNECD-IP PCANGGKCLPFET-QYICKPPGFEHATCKQDINECSQNP PCVHGAPCSVGPDGRFACACPPGTCQSCQSDIDEOR-SG PCENGSTCSSVAN-QFSCKCPAGITGCKCDADINECD-IP PCANGGTCSTLGGSYTCSCLPGYTGTHOLNDTDECAATP PCANGGKCLPFES-SYICGPPGFEHATCKQDINECSQNP </pre>
50		210 220 230 240
55	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> GHCHGGTCLNLPGSYOCQCPQGFTCQYCDSLVPCAPSP GHCHGGTCLNLPGSYOCQCPQGFTCQYCDSLVPCAPSP --CKNGGCQDNEFGSYRCQCONRETCRNCDPEVVPQNPSP TTCRHGGTCLNTPGSFRCCPLGYTGCLLENPVVPCAPSP GRCHGGTCLNLPGSYRCQCPQRFTCQHCDSVPVPCAPSP SICQNEGTCTNTRGSYKCMCALGFTCKHCESSYIPCSPPSP GLCRHGGTCHNEIGSYRCACRATHGPHCELFPVVPQSPSP </pre>
60		250 260 270 280
65	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> CVNGGTCROTCDFTFEC-HLPGFEGSTCERNIDDCPNHRC CVNGGTCROTCDFTFEC-HLPGFEGSTCERNIDDCPNHRC CLNGGTCROTCDFTSYDCCLPGFSGNCEBNIDDCPSNRC CRNGGTCROSSSVYIDCACLPGFEGNCEBNIDDCPSHRC CVNGGTCROTCDFTSECHCLPGFEGNCEBNIDDCPNHRC CLNGGTCNONSTSYSCCLPGFNGNCEBNIDDCPSHRC CONGGTCRPTGDTTHECACLPGFAGNCEBNIDDCPSNRC </pre>
70		290 300 310 320

19

5	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> HPNGYECOCATGFTGVLCERNIDNCDPDPCHHGQCQDGLD HPNGYECOCATGFTGVLCERNIDNCDPDPCHHGQCQDGLD GPNQVTCOCCTEGFTGRHCEODINECHDPDPCHHGTCRDGTA QPDGYECRCATGFEGLCERNVDNCSPPDPCHHGRCVDGTA HPNGYECOCATGFTGTLCDENIDNCDPDPCHHGQCQDGLD LPNGYDCRCATGFKGLCERNINDCVPEPCHHGQCRDGTAA GPNQVTCVCTEGFTGTECEVDIDECDEPDPCHHGTCRDGTA </pre>
10		610 620 630 640
15	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> SYTCICNPGYMGATCSDDQIECYSSPOLNDGRCTDLVNGY SYTCICNPGYMGATCSDDQIECYSSPOLNDGRCTDLVNGY TFTICICRPGYTGRICDNDINECLSKPCLNGGCTDRENGY SFSCACAPGYTGIRCESQVTECRSOPORYGGKCLDLVDKY SYTCICNPGYMGATCSDDQIECYSSPOLNDGRCTDLVNGY TFSCICGYAGYTGATCNIQVECHSNPCONRGCTDLVNAV TFTICICRPGYTGRHCEITNINECHSOPORHGSTCQDRDNYV </pre>
20		650 660 670 680
25	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> QCNCOPGTSGVNCENFDDCASNPCLFGICMDGINRYS CV QCNCOPGTSGVNCENFDDCASNPCLFGICMDGINRYS CV ICTCPKGTIGVNCETKIDDCASNLCQNGKCLDKIDGYECT LRCPPGTIGVNCENFDDCASNPCLFGVCRDGINRYDCV QCNCOPGTSGVNCENFDDCASNPCLFGACVMDGINRYS CV QCNCPPCLSGVNCENFDDCASNLQVNGECQDGINRYKCV LCLCLKGTIGVNCENFDDCASNPCLSGTCLDKIDGYECA </pre>
30		690 700 710 720
35	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> CSPGFTGQRCNTIDECASNPCRKGATCLNGVNGFRCTCP CSPGFTGQRCNTIDECASNPCRKGATCLNGVNGFRCTCP CEPGYTGKLCNTINECDNPNCRNGGCTCKQCLNGFTCVCP CQPGFTGPLCNVINECASFPCEGGGCVLDGNGFHCCLCP CSPGFTGQRCNTIDECASNPCRKDATCLNDVNGFRCTCP CSPGFTGDKCQVINECSSNPQMSGGTCVQNVNGFHCCLCP CEPGYTGSMCNVINECAGCPCHNGGTGEGDGLACFTQRC </pre>
40		730 740 750 760
45	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> EGPHHPSCYSOVNECLSNPCTHGNCTGGLSGYKCLDAGW EGPHHPSCYSOVNECLSNPCTHGNCTGGLSGYKCLDAGW EGYHDMCLSEVNECLSNPCTHGAHDGVNGYKDCIAGW PGSLPPLCLPANHECAHKPCSHGVCHDAPGGFRVCEPGW EGPHHPSCYSOVNECLSSPCTHGNCTGGLSGYKCLDAGW PSTYGLLCLSGTDECVAPCVHKGKTEQONGYFCQCEAGW EGYHDMCLSEVNECLSNPCTHGAHCDGLNGYKDCIAGW </pre>
50		770 780 790 800
55	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> VGINCEV--DKNECLSNPCQNGGTCDNLVNGYRCTCKKGF VGINCEV--DKNECLSNPCQNGGTCDNLVNGYRCTCKKGF SGSNCDL--NNNECESNPCMNGGTCKDNTGAMICTCKAGF SGPRCSQSLAPDACEQPCQAGGTCTSDGIGFRTCTCAPGF VGINCEV--DKNECLSNPCQNGGTCDNLVNGYRCTCKKGF VGQECQO--EKDECLFNPCCNGGSCLDHNGFTCVCOAGY SGINCDL--NNNECESNPCVNGGTCKDNTSGYVCTOREGF </pre>
60		810 820 830 840
65	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	<pre> KGYNCQVNIDECASNPCLNQGTCTDDISGYTCHCVLPYTG KGYNCQVNIDECASNPCLNQGTCTDDISGYTCHCVLPYTG SGPNCQTNINECESNPCLNGTCTDDVAGYKCNCLPYTG QGHQCEV----- KGYNCQVNIDECASNPCLNQGTCTDDVSGYTCHCVLPYTG KGVNCEKNIDECTSGPCLNQGTCTDDGLNSYTCQVPPPTAG SGPNCQTNINECESNPCLNQGTCTDDVAGYKCNCLPYTG </pre>
70		850 860 870 880

5	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	KNCQTVLAPCSNPCEAAVCKESPNTESYTCLCAPGWQG KNCQTVLAPCSNPCEAAVCKESPNTESYTCLCAPGWQG AICSAVLAPCAGSPCKNGGRCKESDDETFCECPFGWQG -----LSPCTPILCEHGGHCESDPR-RLTVCSPPFGWQG KNCQTVLAPCSNPCEAAVCKESPNTESYTCLCAPGWQG EHCSEVLDPCSSRPCORGGVCLPSADYTYTICRCPAGWQG ATCEVVLAPCATSPCKNSGVCKESDYESTSCVCPGTGWQG
10		890 900 910 920
15	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	QRCITDIDDECI-SKPCMNHGLCHNTQGSYMCEPPGFSGM QRCITDIDDECI-SKPCMNHGLCHNTQGSYMCEPPGFSGM QTCEIDMNECV-NRPCRNGATCONINGSYKCNCKPGYTGR PRCCQDMDCEAGASPCGPFGCTCTNLFPENRCHTCHRGYTGP QRCITDIDDECI-SKPCMNHGLCHNTQGSYMCEPPGFSGM LHCSIDVNECK-KNPCRNGCHCINISFSYICRCPGKYSCH QTCEIDMNECV-KSPCRNGASCONINGSYRCLCQAGYTGR
20		930 940 950 960
25	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	DCEEDIDDDCLASPCONGGSCMDGVNMFSCCLCPGFTGDKC DCEEDIDDDCLANPCONGGSCMDGVNMFSCCLCPGFTGDKC NCCEIDDDCDQNPCENGGSCSDGINMFCNCPACERGPAC FCIQDIDDDCDNPCLGGGSCODGVGSEFSCSCLDGFAGPFC DCEEDIDDDCLANPCONGGSCVDKVNMFSCCLCPGFTGDKC NCQDIDDDCSNPCLNGGSCVDDVGFSECECRPGEGEGHC NCESDIDDCRNPCENGGSCDGVNAAFCDCLPGFQGAFC
30		970 980 990 1000
35	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	QTDINECLSEPCRNNGGTCSDVNSYTCKCQAGFDGVHCEN QTDINECLSEPCRNNGGTCSDVNSYTCKCQAGFDGVHCEN EEDINECASNPCKNGANCDCVNSYTCTCPGFSCTHCE ARDVIECLSSPGGFG-TCIDEVASFTACPPSYGGFHCET QTDINECLSEPCRNNGGTCSDVNSYTCTCPAGFEGVHCEN EIADECASOPCKNGATCRDVNSYVCECRLGEGDGHLCDE EEDINECATNPCKNGANCDCVNSYTCTCPGFSCTHCE
40		1010 1020 1030 1040
45	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	NINECTESSCFNGGTCVDGINSFSCLCPVGFTGSEFCLHET NINECTESSCFNGGTCVDGINSFSCLCPVGFTGSEFCLHET NTPCTESSCFNGGTCVDGINTFTCTCPGFTGSEFCLHET DTPCTESSCFNGGTCVDGVNFSCLCPVGFTGSEFCLHET NINECTESSCFNGGTCVDGINSFSCLCPVGFTGSEFCLHET NINECTESSCFNGGTCVDGINTFTCTCPGFTGSEFCLHET NTPCTESSCFNGGTCVDGINSFSCLCPVGFTGSEFCLHET
50		1050 1060 1070 1080
55	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	NECSSHPCLNDGTCVDGLTYRCSCLPGYTGKNCQTLVNL NECSSHPCLNEGTCVDGLTYRCSCLPGYTGKNCQTLVNL NECDSKPCLNNGGTCQDSYCTYKCTCPGYTGKNCQTLVNL DPCFSRPLNGGTCQDSYCTYKCTCPGYTGKNCQTLVNL NECSSHPCLNSCTCVDGLTYRCSCLPGYTGKNCQTLVNL NECDSOPCKNGGTCQDSYCTYKCTCPGYTGKNCQTLVNL NECDSRPLNGGTCQDSYCTYKCTCPGYTGKNCQTLVNL
60		1090 1100 1110 1120
65	MOL1a MOL1b gi 104252 gi 6679096 gi 13242247 gi 2209059 gi 6093542	CSRSPPCKNKGTCVOKKARS-QCLCPSGWAGAYCDVFNVSC CSRSPPCKNKGTCVOKKARS-QCLCPSGWAGAYCDVFNVSC CDSPPCKNKGTCVOKKARS-QCLCPSGWAGAYCDVFNVSC CSQAPCKNGGTCVOKKARS-QCLCPSGWAGAYCDVFNVSC CSRSPPCKNKGTCVOKKARS-QCLCPSGWAGAYCDVFNVSC CRQVRCKNGGTCVOKKARS-QCLCPSGWAGAYCDVFNVSC CDSPPCKNKGTCVOKKARS-QCLCPSGWAGAYCDVFNVSC
70		1130 1140 1150 1160

	MOL1a	DIASRRGVLEHLCOHSGYCTINAGNTHYCCPLGYTGSY
	MOL1b	DIASRRGVLEHLCOHSGYCTINAGNTHYCCPLGYTGSY
5	gi 104252	EVAAKQCGVDLVEHLCOHSGYCTINAGNTHYCCPLGYTGSY
	gi 6679096	TEAAACMGVRLLEHLCOHSGYCTINAGNTHYCCPLGYTGSY
	gi 13242247	KAAALQKGVPLVEHLCOHSGYCTINAGNTHYCCPLGYTGSY
	gi 2209059	RDFAARKGLTEELVEHLCOHSGYCTINAGNTHYCCPLGYTGSY
	gi 6093542	EVAAKQCGVDLVEHLCOHSGYCTINAGNTHYCCPLGYTGSY
10		1170 1180 1190 1200
	MOL1a	CEEQIDECASNFCQEGATCDDYLGGRCECVPGYCGVNCE
	MOL1b	CEEQIDECASNFCQEGATCDDYLGGRCECVPGYCGVNCE
15	gi 104252	CEEQIDECASNFCQEGATCDDYLGGRCECVPGYCGVNCE
	gi 6679096	CEEQIDECASNFCQEGATCDDYLGGRCECVPGYCGVNCE
	gi 13242247	CEEQIDECASNFCQEGATCDDYLGGRCECVPGYCGVNCE
	gi 2209059	CEEQIDECASNFCQEGATCDDYLGGRCECVPGYCGVNCE
	gi 6093542	CEEQIDECASNFCQEGATCDDYLGGRCECVPGYCGVNCE
20		1210 1220 1230 1240
	MOL1a	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
	MOL1b	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
25	gi 104252	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
	gi 6679096	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
	gi 13242247	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
	gi 2209059	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
	gi 6093542	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
30		1250 1260 1270 1280
	MOL1a	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
	MOL1b	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
35	gi 104252	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
	gi 6679096	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
	gi 13242247	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
	gi 2209059	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
	gi 6093542	YEVDECONQPCQNGGTCIDLVMHFKCSCPPGTRGMKSSLS
40		1290 1300 1310 1320
	MOL1a	ERCEGDINECLSNPCSSSEGLDCTQLLN--DYLCVCRSAFT
	MOL1b	ERCEGDINECLSNPCSSSEGLDCTQLLN--DYLCVCRSAFT
45	gi 104252	ERCEGDINECLSNPCSSSEGLDCTQLLN--DYLCVCRSAFT
	gi 6679096	ERCEGDINECLSNPCSSSEGLDCTQLLN--DYLCVCRSAFT
	gi 13242247	ERCEGDINECLSNPCSSSEGLDCTQLLN--DYLCVCRSAFT
	gi 2209059	ERCEGDINECLSNPCSSSEGLDCTQLLN--DYLCVCRSAFT
	gi 6093542	ERCEGDINECLSNPCSSSEGLDCTQLLN--DYLCVCRSAFT
50		1330 1340 1350 1360
	MOL1a	GRHCEHFDVCPQMPCLNGGTCAVASNMPDGS--FAVVPQ
	MOL1b	GRHCEHFDVCPQMPCLNGGTCAVASNMPDGS--FAVVPQ
55	gi 104252	GRHCEHFDVCPQMPCLNGGTCAVASNMPDGS--FAVVPQ
	gi 6679096	GRHCEHFDVCPQMPCLNGGTCAVASNMPDGS--FAVVPQ
	gi 13242247	GRHCEHFDVCPQMPCLNGGTCAVASNMPDGS--FAVVPQ
	gi 2209059	GRHCEHFDVCPQMPCLNGGTCAVASNMPDGS--FAVVPQ
	gi 6093542	GRHCEHFDVCPQMPCLNGGTCAVASNMPDGS--FAVVPQ
60		1370 1380 1390 1400
	MOL1a	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF
	MOL1b	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF
65	gi 104252	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF
	gi 6679096	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF
	gi 13242247	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF
	gi 2209059	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF
	gi 6093542	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF
70		1410 1420 1430 1440
	MOL1a	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF
	MOL1b	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF
	gi 104252	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF
	gi 6679096	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF
	gi 13242247	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF
	gi 2209059	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF
	gi 6093542	GFSGARC---QSSCGQVKCRKGEQCVHTASGPRCFQPSF

	
	MOL1a	R-----DCE-----SGC-----A-SSEPCQGGSCHPQQRQ-
	MOL1b	-----
5	gi 104252	YTG--ATCQYPTVISP-----A-SHPCYNGGTGCOFFAEE
	gi 6679096	LSG--PSCRVSRAVSPSGATNASCASAPCLEGGSCLPVQSV
	gi 13242247	K-----DCE-----SGC-----A-SNPCCQGGTCYPQQRQ-
	gi 2209059	QGFSGAHCEN-----SQW-----C-PWPCQNGGTCKMKDSAN
	gi 6093542	FTG--PECQFPASSPC-----VGSNCPYNGGACCEPTSES
10		1450 1460 1470 1480
	MOL1a	PPFYSCCCAPPESGSRCELY-----TAPPSTPFA-----T
	MOL1b	-----FTCRCPPEGEG-----
15	gi 104252	P-EEQCFQPKNENGLFCHILDYEFPPGGLGKNITEPDNDI
	gi 6679096	P-ETRCVCAPGCGGPRCETP-----SAAPEVPEEP-----R
	gi 13242247	PPYYSQRCSPPEWGHCESY-----TAPTSTPFA-----T
	gi 2209059	PVQYSCHCNNESGRYCENN-----VVGSG--PS-----T
	gi 6093542	P-FYRCLCPAKENGLLCHILDYSFTGAAGRDIPEPQIEEA
20		1490 1500 1510 1520
	MOL1a	CLSQYCADKERRGCVDEACNSHACQNDGGDCSLTMEHPWA
	MOL1b	-----
25	gi 104252	CENEQCSSELADNKNCMANCMNEACQNDGGDCSLNFNBPWK
	gi 6679096	CPRAACQAKRGDQNDRECNTPGCGNDGGDCSLNVDPPWR
	gi 13242247	CLSQYCADKERRGCVDEACNSHACQNDGGDCSLTMEHPWA
	gi 2209059	CPYLOCKHHSADKQDAOCNNHECQNDGGDCSLNWKQPS
	gi 6093542	CELPEQEDAGNKVCNLOCMNEACQNDGGDCSLNFNBPWK
30		1530 1540 1550 1560
	MOL1a	NCSSTLPQWDYINN-CCDELCNTVECLFDNFECCG--NSK
	MOL1b	-----
35	gi 104252	NCTQSLQCNKYFSDGHCDSQCNNTGCLYDGFDCCK--VEV
	gi 6679096	QC-KALQCNRLFNNSRCDPACSSPACLYDNFECYSGGRDR
	gi 13242247	NCTSSLRCEYIINN-CCDELCNTVECLFDNFECCG--NSK
	gi 2209059	NCTASYSQWDLFKNGRCDKECONPGCLFDGFDCCK--H-K
	gi 6093542	NCTQSLQCNKYFSDGHCDSQCNNSAGCLFDGFDCQL--TEG
40		1570 1580 1590 1600
	MOL1a	TCK--YDKYCADHFRDNHCECGCNSRECCGWDGLDCAADQ
	MOL1b	-----
45	gi 104252	QCNPLMDQYCKDHFSDGHCDCGCSNAECGWDGLDCAN-M
	gi 6679096	TCNPFVMEKYCADHFRDNCDCGCSNECCGWDGLDCASEVP
	gi 13242247	TCK--YDKYCADHFRDNHCECGCNSRECCGWDGLDCAADQ
	gi 2209059	TCKYVMEKYCADHFRGNKICDPSCTYKACGWDGLDCAGDT
	gi 6093542	QCNPLMDQYCKDHFSDGHCDCGCSNAECGWDGLDCAEHVP
50		1610 1620 1630 1640
	MOL1a	ENLAECTLVIVVLMPPPEQLLODARSFLRALGTLLETNLRI
	MOL1b	-----
55	gi 104252	ENLAECTLVIVVLMPPPERLKNNSVNFLELSRYLHTNVVF
	gi 6679096	ALLARGVLVLTVLLPPEELRSSADFLRLSALRLTSLRF
	gi 13242247	ENLAECTLVIVVLMPPPEQLLODARSFLRALGTLLETNLRI
	gi 2209059	AKIVPGTLVIVVLPKELGDLRGFLRLSGALTYTNQV
	gi 6093542	ERLAECTLVIVVLMPPDQLRNSFHLRLDVSHLHTNVVF
60		1650 1660 1670 1680
	MOL1a	KRDSQGEHLMVYPYCEKSAAMKKQMT-----
	MOL1b	-----
65	gi 104252	KRDSRGEYKLYPYTCNEEELKKHHIKRSTDYNSDAPSAIF
	gi 6679096	RLDARGQAMVFPYERPSPGS-----
	gi 13242247	KRDSQGALMVYPYCEKSAAMKKQKVA-----
	gi 2209059	KLDENNKPMVYPYFGVENHG--QQLK-----
	gi 6093542	KRDAQGQOMIFPYICREELRKHPIKRSAVGWATT-----
70		1690 1700 1710 1720

5

10

15

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55

60

65

70

MOL1a
MOL1b
gi|104252|
gi|6679096|
gi|13242247|
gi|2209059|
gi|6093542|

RRSLPGEQEQEVAGSKVFLEIDNRQCVQDSD
STMKESILLGRHRRELDENVRGSIIVYLEIDNRQCYKSSS
-----ESSRVRRELGPENIGSVVMLEIDNRQLQCSAE
-----RRSLPDEQEQETIGSKVFLEIDNRQCVQDSD
-----GSRSKRELEKEVIGSVVBLEIDNRKCSKSSG
-SLLPGTNGGRQRRLDPMDEEGSIIVYLEIDNRQCVQSSS

1730 1740 1750 1760
.....|.....|.....|.....|.....|.....|
--ECNKNTDAANALASHATOGTIS--YPLVSVVSESLT
MOL1a
MOL1b
gi|104252|
gi|6679096|
gi|13242247|
gi|2209059|
gi|6093542|

-----OCENSATDVBAFLGALASLGSIIDTLSKRREAVKSENME
NDECHPDAQSAEDYLGALSAVEREDFP-YPLKRDVRGEPLE
--OCNKNTDAANALASHATOGTIS--YPLVSVVSESED
--ECFSKTEEVASTLAAAHKADLP--YPLVSVVNSPAV
--OCQSATDVBAFLGALASLGSIIN-IPYKREAVKSETVE

1770 1780 1790 1800
.....|.....|.....|.....|.....|.....|
PE--RTOLLYLNAVAVVTHIFITLGVVMA-KRRRHGSE
MOL1a
MOL1b
gi|104252|
gi|6679096|
gi|13242247|
gi|2209059|
gi|6093542|

TPPKSTLYPMCSMLVIPLEHIFVFMVIVNKKRRRHDSF
APEQSVPLLPGLVAGAVYHIFITGVVVA-KRRRHSTL
PR--NTPLLYLNAVAVVTHIFIDLVVMA-KRRRHGFL
PIRETHILPYLVGVSVVLEHIVLVGLAA-KRRKHGGL
PPLPSQLHLMYAAAAFVLEFFVGC SVLISKRRRHGOL

1810 1820 1830 1840
.....|.....|.....|.....|.....|.....|
NLPEGEFLRRDASN--HKRREEVGGDVAVLKNLVQVNSEA
MOL1a
MOL1b
gi|104252|
gi|6679096|
gi|13242247|
gi|2209059|
gi|6093542|

GSPTALFQKN-PKK--RNG-ETPNEDSVGLKP-LKNMTDG
NPEGEFALHKDIAAGHKGRREEVGGDVAIGMKN---MAKG
NLPEGEFLRRDASN--HKRREEVGGDVAVLKNLVQVNSEA
NLPEGEFMANK---N--DKRREEVGGDIDFLKN--FKTQDG
NPEGEFKVSE-ASK--KKRREPLGEDSVGLKP-LKNASDG

1850 1860 1870 1880
.....|.....|.....|.....|.....|.....|
NLGTGTTHHHVDDG-GPOPKKVKAEDDEALLSESDPIDR
MOL1a
MOL1b
gi|104252|
gi|6679096|
gi|13242247|
gi|2209059|
gi|6093542|

SFDDDNONE-WGDEE-TLENKFRFEEQVILPELVDDKTD
ESLMGEVVTDLNDSECPKAKLKVVEPG---MGAKRPEDC
NLGTGTTSEHWDDE-GPOPKKAKAEDDEALLSESDPVDR
AVLDGGQDORMLDE-VPPRKPRLEGGKPLLPMAAGGVDR
ALDDDNONE-WGDEE-LETKKFRFEEPVVLPDL-DQQTDH

1890 1900 1910 1920
.....|.....|.....|.....|.....|.....|
RPNTQOHLDAADIRRTPSLALTPPOAEQEVVDVLDVNRGP
MOL1a
MOL1b
gi|104252|
gi|6679096|
gi|13242247|
gi|2209059|
gi|6093542|

ROWTROHLDAAADLR-ISEMAPPTPQGEVADCDVNRGP
ROWTROHLLVAADIRVAPATALETPPOQDADAGVDVNRGP
RPNTQOHLDAADIRRTPSLALTPPOAEQEVVDVLDVNRGP
ROWTROHRLAADIS-----LTPPOAELISDGVVDVNRGP
ROWTROHLDAAADLR-VSEMAPTPPQGEVADCDVNRGP

1930 1940 1950 1960
.....|.....|.....|.....|.....|.....|
DGFTPLMLASLRGG---SSDLSDDED---AEDSSANTIT
MOL1a
MOL1b
gi|104252|
gi|6679096|
gi|13242247|
gi|2209059|
gi|6093542|

DGFTPLMLASCSGG---GLGTGNSSEE---EDASAMIS
DGFTPLMLASFCGG---ALPMPAEDE---ADDTASITIS
DGCTPLMLASLRGG---SSDLSDDED---AEDSSANTIT
DGFTPLMLASLRNGGVLDCLNGDFEESGGEPPGSSVLS
DGFTPLMLASCSGG---GLGTGNSSEE---EDAPA VLS

1970 1980 1990 2000
.....|.....|.....|.....|.....|.....|

	MOL1a
	MOL1b	DLVYQGASLQAQTDRTGEMALHLAARYSRADAARKRLLDAG
5	gi 104252	DLVYQGAQLHNTDRTGETALHLAARYSRADAARKRLLESS
	gi 6679096	DLVYQGAQLGARTDRTGETALHLAARYSRADAARKRLLDAG
	gi 13242247	DLVYQGASLQAQTDRTGEMALHLAARYSRADAARKRLLDAG
	gi 2209059	DLVYQGAQLQAQTDRTGETALHLAARYSRADAARKRLLDAG
	gi 6093542	DLVYQGAQLHNTDRTGETALHLAARYSRADAARKRLLESS
10		2010 2020 2030 2040
	MOL1a
	MOL1b	ADANAQDNMGRCPHAAVADAAQGVFQILIRNRVTDLDAR
15	gi 104252	ADANVQDNMGRCPHAAVADAAQGVFQILIRNRATDLDAR
	gi 6679096	ADANAQDNMGRCPHAAVADAAQGVFQILIRNRSTDLAR
	gi 13242247	ADANAQDNMGRCPHAAVADAAQGVFQILIRNRVTDLDAR
	gi 2209059	ADANAQDNMGRCPHAAVADAAQGVFQILIRNRATDLDAR
	gi 6093542	ADANAQDNMGRCPHAAVADAAQGVFQILIRNRATDLDAR
20		2050 2060 2070 2080
	MOL1a
	MOL1b	MNDGTTPLILAAARLAVEGMVAELINCAADVNAVDDHGKSA
25	gi 104252	MNDGTTPLILAAARLAVEGMVAELINCAADVNAVDDHGKSA
	gi 6679096	MNDGTTPLILAAARLAVEGMVAELINCAADVNAVDDHGKSA
	gi 13242247	MNDGTTPLILAAARLAVEGMVAELINCAADVNAVDDHGKSA
	gi 2209059	MNDGTTPLILAAARLAVEGMVAELINCAADVNAVDDHGKSA
	gi 6093542	MNDGTTPLILAAARLAVEGMVAELINCAADVNAVDDHGKSA
30		2090 2100 2110 2120
	MOL1a
	MOL1b	LHWAAAVNNVFAVLLKNGANKDMONKEETPLFLAARE
35	gi 104252	LHWAAAVNNVFAVLLKNGANKDMONKEETPLFLAARE
	gi 6679096	LHWAAAVNNVFAVLLKNGANKDMONKEETPLFLAARE
	gi 13242247	LHWAAAVNNVFAVLLKNGANKDMONKEETPLFLAARE
	gi 2209059	LHWAAAVNNVFAVLLKNGANKDMONKEETPLFLAARE
	gi 6093542	LHWAAAVNNVFAVLLKNGANKDMONKEETPLFLAARE
40		2130 2140 2150 2160
	MOL1a
	MOL1b	GSYEAAKLLDHFANRDITDHDRLPRDVAQERMHHDIVR
45	gi 104252	GSYEAAKLLDHFANRDITDHDRLPRDVAQERMHHDIVR
	gi 6679096	GSYEAAKLLDHFANRDITDHDRLPRDVAQERMHHDIVR
	gi 13242247	GSYEAAKLLDHFANRDITDHDRLPRDVAQERMHHDIVR
	gi 2209059	GSYEAAKLLDHFANRDITDHDRLPRDVAQERMHHDIVR
	gi 6093542	GSYEAAKLLDHFANRDITDHDRLPRDVAQERMHHDIVR
50		2170 2180 2190 2200
	MOL1a
	MOL1b	LLDEYNVTPSPPG--TVLTSA--LSP-VICGPNRS-FL-S
55	gi 104252	LLDEYNLVKSPFLHNGPLGAT-TLSP-PLCSPNG--YMGK
	gi 6679096	LLDQPSGPRSPS---GPHG---LSP-LLCPPG--AFIPG
	gi 13242247	LLDEYNVTPSPPG--TVLTSA--LSP-VICGPNRS-FL-S
	gi 2209059	LLDEYNVHSPHNGPNLGGGA--GNPSMCGANGAGFM-N
	gi 6093542	LLDEYNVVRSPQLHGTAAGGTPTLSP-TLCSPNG--YLGK
60		2210 2220 2230 2240
	MOL1a
	MOL1b	LKHTPMG-KKSRPPSAKSTMPSTSLPNLAKEAKDAKGSRRK
65	gi 104252	LKPSVQS-KKARKPSIK-----GNGC--KEAKELKARRKK
	gi 6679096	LKAVQSCTKKSRPPCK-----TGLG--PGTRGRGRKK
	gi 13242247	LKHTPMG-KKARKPPSTKSTMPSTSLPNLAKEAKDAKGSRRK
	gi 2209059	VRSGAQQ-KKRRGGGGVTVNG-VVGGGPKELKMKSKRRK
	gi 6093542	LKSAQCG-KKARKPSIK-----GLACSSKEAKELKARRKK
70		2250 2260 2270 2280

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      .....|.....|.....|.....|.....|.....|.....|.....|
MOL1a KSLSEKVQLS-ESSVTLSFVDSLESPTIVSDTSSPMIT
MOL1b
5 gi|104252| SQDGKTTLLDSCSSGVLSFVDSLESTHGYSLVSSPPLMT
  gi|6679096| -----LTHA
  gi|13242247| KCLNEKVQLS-ESSVTLSFVDSLESPTIVSDATSSPMIT
  gi|2209059| KPTG--VEGP-GASAGAG--G-----AIGGTAANGTN
  gi|6093542| SQDGKGCILLD--SSMLSFVDSLESPPHGYSLVSSPPLMT

      2290      2300      2310      2320
MOL1a .....|.....|.....|.....|.....|.....|.....|.....|
MOL1b .....|.....|.....|.....|.....|.....|.....|.....|
15 gi|104252| EEFQQSFSMPLNHLTSMDEEOLGMNHINMATKQEMAAGS-
  gi|6679096| CPG-----PLADSSVTLSFVDSLDSPRPFGSP-
  gi|13242247| EFGILQASPTP-LLAAAEAPVHAQHLSFSNLHEMQPL-
  gi|2209059| ANGVKTAG-----ALPESSVTMTSPVDSLESPPHSFLGD-
  gi|6093542| EEFQQSFSMPLSHLPGLDTHLIGISHLNVAAPKPEMAALAG

      2330      2340      2350      2360
MOL1a --AHGASTVLESVSOLL--SHHHTVSPG--SGSAGSLSR
MOL1b
25 gi|104252| -NRMAFDAMVRLTHIN-ASSPNTTMSN--GSMHFTYCG
  gi|6679096| --PASPGGFPLEGPTYATTATAVSLAQLG--ASRAGPEGR
  gi|13242247| --RPGASTVLESVSOLL--SHHHTVPPG--SGSAGSLSR
  gi|2209059| --VSGTVSTTANSPPL--SSPTTRPML--PPVSHMLCQ
  gi|6093542| GSRLAFEPFPPRLSHLPVASSASTVLTSTNGTGAMNFTVCA

      2370      2380      2390      2400
MOL1a LHPVPVPADANRMEVNETQYNEMEGMVLAPAV-GH--PS
MOL1b
35 gi|104252| APTMNSQCDNLAR--LONGMVONQEDFERNGIQQGN-AQQ
  gi|6679096| QP-----PGG-----
  gi|13242247| LHSVVPVSDANRMEVNETQYSEMEGMVLAPAEGR--PG
  gi|2209059| QQ-----G-IVG--TTKHPYSDHMSLTPHQIGGSH--TG
  gi|6093542| PASLNGQCEALPR--LONGMVPSQNLPRPGVTPGTLSTQ

      2410      2420      2430      2440
MOL1a WHSSPERPPEGKHITTPREPPLPPTFGLPKG-----
MOL1b
45 gi|104252| AQALQHGMLTSLNGLPATTLSOMTYQAMPNTRLANQPH
  gi|6679096| -CVLSFGLLNPFVAVPLDWARLPP-----
  gi|13242247| MAAPQSRAPGKPIPTQREPLPPTFVTFGLPKG-----
  gi|2209059| MGHSRGPMFTPMNVTMSRECLPPTVFQMAPGGGQGMK
  gi|6093542| AAGLQHGMMGPIHSSLSNTLSPLT-XQGPNTRLATQPH

      2450      2460      2470      2480
MOL1a -----SIA-----QPAGAPQPQSTCPPAVAGPLP
MOL1b
55 gi|104252| LMQAQQMQQQ-----QNLQLHQSMQQQHNSSTTSTHINSP
  gi|6679096| -----SLA-----QAAGAPQTQSGCPPAVAGPLP
  gi|13242247| QSQTGQVQVT-----QSQNQSHSQG-PGHLHCAQS
  gi|2209059| LVQTQVQVQNLQIQPNLQPPSQPHLSVSSAANGHLGRS
  gi|6093542|

      2490      2500      2510      2520
MOL1a TMYQIDEMARLPS-----VAFPTAMPEQDQGVACT-ILP
MOL1b
65 gi|104252| --YQIDEMARLPS-----VAFPTAMPEQDQGVACT-ILP
  gi|6679096| FCSSDISQTDIQMS--SNNIHSVPEQDTQIFAAS--EP
  gi|13242247| --PAPPGPSFLP-----VAPGPQLNPGAPVSPCE-RP
  gi|2209059| SMYQIDEMARLPS-----VAFPTAMPEQDQGVACT-IVP
  gi|6093542| MMYQMNEMQMGHGLPHTVQHPHTIGHGHAGMEGQSRQLP
  FLSGEPSCADVQPLGP-SSLPVHTLPEQESQALPTS--LP

      2530      2540      2550      2560

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	MOL1a	AMHPPASVGVKYPPTPSQHSYASSNAAERTTPSHSGHLOGE
	MOL1b	AMHPPASVGVKYPPTPSQHSYASSNAAERTTPSHSGHLOGE
5	gi 104252	SNLTQSMITTAQELTPPSQHSYSS--PMDNTPSHQLOVP-D
	gi 6679096	PHLAAPGHGEEYPAAGTRSSPTK-----ARFLRMPSE
	gi 13242247	AMHPPASVGVKYPPTPSQHSYASSNAAERTTPSHSGHLOGE
	gi 2209059	SMQPMQSPVDKYPTPSQHSYTTGSGEGTTPGHSAPHPSE
	gi 6093542	SMVPEMTTQELTPPSQHSYSSS-PVDMTPSHQLOVP-E
10		2570 2580 2590 2600
	MOL1a	HPYLTPSPESPDQWSSSSPHS-ASDWSDEVTSPTPGG---
	MOL1b	HPYLTPSPESPDQWSSSSPHS-ASDWSDEVTSPTPGG---
15	gi 104252	HPYLTPSPESPDQWSSSSPHSNMSDWSRGISSP-----
	gi 6679096	HPYLTPSPESPEHWASESPLES-LSDWSDSPTSPATATNAT
	gi 13242247	HPYLTPSPESPDQWSSSSPHS-ASDWSDEVTSPTPGG---
	gi 2209059	HPYLTPSPESPDQWSSSSPHS-NSDWSDEVTSPTPLGNLT
	gi 6093542	HPYLTPSPESPDQWSSSSPHSNISDWSRGISSP-----
20		2610 2620 2630
	MOL1a	-----AGGGQRGEGTHMSEEPHNNMQVYA-
	MOL1b	-----AGGGQRGEGTHMSEEPHNNMQVYA-
25	gi 104252	-----TSMQPORTHIEKAFK-----
	gi 6679096	ASGALPAQPHPISVPSLPQSQTQLGQCEVTPPKRQVMA
	gi 13242247	-----GGGGQRGEGTHMSEEPHNNMQVYA-
	gi 2209059	THCRLETAHTFQSRCS CSPSENRF SRAE SSSLWGTCR-
	gi 6093542	-----TSMESQITHIEKAFK-----
30		

When the sequences of the invention are referred to as MOL1, this refers to the sequences disclosed as MOL1a and MOL1b.

The presence of identifiable domains in MOL1, as well as all other MOLX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (<http://www.ebi.ac.uk/interpro>). DOMAIN results, e.g., for MOL1 as disclosed in Table 1I, were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections. For Table 1I and all successive DOMAIN sequence alignments, fully conserved single residues are indicated by black shading and "strong" semi-conserved residues are indicated by grey shading. The "strong" group of conserved amino acid residues may be any one of the following groups of amino acids: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW.

Tables 1I-1N list the domain description from DOMAIN analysis results against MOL1. The region from amino acid residue 1416 through 1454 (SEQ ID NO:2) most probably ($E = 1e^{-6}$) contains a domain found in Notch and Lin-12, aligned here in table 1I. Notch and Lin-12 are both involved in organismal development, cell cycle, and apoptosis. The region from amino acid residue 1504 through 1532 (SEQ ID NO:2) most probably ($E = 2e^{-4}$) also contains a domain found in Notch and Lin-12, aligned here in table 1J. The region from

amino acid residue 1875 through 1906 (SEQ ID NO:2) most probably ($E = 6e^{-5}$) contains an Ank repeat, aligned here in table 1K. Ank repeats are markers for the protein ankyrin which is involved in cell adhesion and contact inhibition. The region from amino acid residue 1974 through 2006 (SEQ ID NO:2) most probably ($E = 2e^{-4}$) also contains an Ank repeat, aligned here in table 1L. The region from amino acid residue 182 through 215 (SEQ ID NO:2) most probably ($E = 1e^{-4}$) contains a Calcium binding EGF-like domain, aligned here in table 1M. EGF is a growth factor that modulates the proliferation of many cell types. The region from amino acid residue 872 through 908 (SEQ ID NO:2) most probably ($E = 9e^{-4}$) also contains a Calcium binding EGF-like domain, aligned here in table 1N. This indicates that the MOL1 sequence has properties similar to those of other proteins known to contain these domains.

Table 11. Domain Analysis of MOL1

gnl|Smart|smart00004, NL, Domain found in Notch and Lin-12; The Notch protein is essential for the proper differentiation of the Drosophila ectoderm. This protein contains 3 NL domain
CD-Length = 39 residues, 100.0% aligned
Score = 50.1 bits (118), Expect = 1e-06

10 20 30 40
 MOL1_1 PSIPPTATCL---SOYCADKARDGVCDEACNSHACQWDGGDCS
 Smart|smart00004 PQDPWSRCK---DAQCWDKFGDGVCDDEECNAECLFDGGDCS (SEQ ID NO:83)

Table 1J. Domain Analysis of MOL1

gnl|Smart|smart00004, NL, Domain found in Notch and Lin-12; The Notch protein is essential for the proper differentiation of the Drosophila ectoderm. This protein contains 3 NL domains
CD-Length = 39 residues, only 74.4% aligned
Score = 43.1 bits (100), Expect = 2e-04

Score = 43.1 Bits (100%)

MOL1_2
Smart|smart00004

.....10.....20.....30.....40.....
FECQGN SKTKYDKYCADHFKDNECDQGCNSECCWDGLDCA
PODPWRCED---DAQQWDKFGDGVCDESCNNAECLWDGGDCS (SEQ ID NO:84)

Table 1K. Domain Analysis of MOL1

gnl|Pfam|pfam00023, ank, Ank repeat
CD-Length = 33 residues, 97.0% aligned
Score = 44.7 bits (104), Expect = 6e-05

MOL1_3
 Pfam|pfam00023

TGEALHHLAARYS...RADAARLLD...AGADANAQDN
 DGNTPHHLAARNG...HLEVVKLLLE...AGADVNRDK (SEQ ID NO:85)

Table 1L. Domain Analysis of MOL1

gnl|Pfam|pfam00023, ank, Ank repeat
CD-Length = 33 residues, 100.0% aligned
Score = 43.1 bits (100), Expect = 2e-04

MOL1_4 HGKSAIHWAPAVNNVEATLILLK-NGANRDMQDN
Pfam|pfam00023 DGNTPPLHLAARNGHLEVVKKILLK-ACADVNRDK (SEQ ID NO:86)

Table 1M. Domain Analysis of MOL1

```
gnl|Smart|smart00179, EGF_CA, Calcium-binding EGF-like domain
CD-Length = 41 residues, 85.4% aligned
Score = 43.5 bits (101), Expect = 1e-04
```

10 20 30 40 50
 MOL1_7 DVNECDIP-----GHCHGGGTCTNLPGSYOC-CCPCGCTGQYCDSLYV
 Smart smart00179 DIPECASG-----NPCCGGCTCYNTVGSYRCRCPCPPGYLD--GRNCE

MOL1_7
Smart|smart00179 (SEQ ID NO:87)

Table 1N. Domain Analysis of MOL1

```

gnl|Smart|smart00179, EGF_CA, Calcium-binding EGF-like domain
CD-Length = 41 residues, 100.0% aligned
Score = 40.8 bits (94), Expect = 9e-04

```

10 20 30 40 50
 MOL1_8 DIDECISK-----PCMHGELCHNTGSSYMC-ECPPGSGSGMPC
 Smart|smart00179 DIDECASG-----NPCNGGCTGVNTVGSYRCFECPPGCTL--DGRNC

MOL1_8 E
Smart|smart00179 E (SEQ ID NO:88)

Uses of the Compositions of the Invention

The protein similarity information, expression pattern, cellular localization, and map location for the protein and nucleic acid disclosed herein suggest that MOL1 may have important structural and/or physiological functions characteristic of the EGF-like domain-containing protein family. Therefore, the nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications and as a research tool. These include serving as a specific or selective nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These also include potential therapeutic applications such as the following: (i) a protein therapeutic, (ii) a small molecule drug target, (iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a nucleic acid useful in gene therapy (gene delivery/gene

ablation), (v) an agent promoting tissue regeneration *in vitro* and *in vivo*, and (vi) a biological defense weapon.

The MOL1 nucleic acids and proteins have applications in the diagnosis and/or treatment of various diseases and disorders. For example, the compositions of MOL1 may have efficacy for the treatment of patients suffering from endometriosis, fertility disorders, cancer, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, systemic lupus erythematosus, asthma, emphysema, scleroderma, allergy, ARDS, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, multiple sclerosis, ulcers, ataxia-telangiectasia, leukodystrophies, behavioral disorders, addiction, anxiety, pain, neuroprotection, osteoporosis, hypercalceimia, arthritis, ankylosing spondylitis, scoliosis, diabetes, autoimmune disease, myasthenia gravis, muscular dystrophy, renal artery stenosis, interstitial nephritis, glomerulonephritis, polycystic kidney disease, systemic lupus erythematosus, renal tubular acidosis, IgA nephropathy, hypercalceimia, Lesch-Nyhan syndrome, developmental disorders, growth disorders, and/or wounds, as well as other diseases, disorders and conditions. The reactivation of the Notch signaling pathway during wound healing has been demonstrated and the similarity between developmental and regenerative processes has been suggested (*Exp Cell Res* 1999 Feb 1;246(2):312-8).

These materials are further useful in the generation of antibodies that bind immunospecifically to the novel MOL1 substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-MOLX Antibodies" section below. The disclosed MOL1 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated MOL1 epitope is from about amino acids 10 to 150. In another embodiment, a MOL1 epitope is from about amino acids 160 to 190. In additional embodiments, MOL1 epitopes are from about amino acids 195 to 350, 400 to 525, 550 to 575, 590 to 600, 610 to 650, 780 to 880, 900 to 1000, 1100 to 1150, 1175 to 1200, 1225 to 1300, and from about amino acids 1380 to 1500. These novel proteins can also be used to develop assay systems for functional analysis.

MOL2

MOL2 is a novel insulin-like growth factor binding protein-like protein. The novel nucleic acid of 2631 nucleotides, (SC98428706_EXT, SEQ ID NO:5) encoding a novel insulin-like growth factor binding protein-like protein is shown in Table 2A. The start and stop codons are in bold.

Table 2A. MOL2 Nucleotide Sequence (SEQ ID NO:5)

```

ATGATTACATACAAGTAATTTTCAAGTAATGACCATTGAAAAATGTTTCTTTTATTATTTTAGATTATTTCTC
TTTATTTCAGAAGCATACAGTTGTTTGTCTGATTGCAAGAAGATGTTTCTGTGGCTGTTTCTGATTTTGTGAGCCCTGA
TTTCTTCGACAAATGCAGATTCTGACATATCGGTGGAATTTGCAATGTGTGTTCTTGCCTGTGAGTGTGAGTGTG
CTCTATGTCAACTGTGAGAAGGTTTCAGTCTACAGACCAAATCAGCTGAAACCACCTTGGTCTAATTTTATCACT
CAATTTCCAAAATAATTTTAAATATTCTGTATCCAAATACATTCTTGAATTTTTCACATGCAGTCTCCCTGCATC
TGGGGAATAATAAAGTGCAGAACATTGAGGGAGGAGCCTTTCTTGGGCTCAGTGCATTAAAGCAGTTGCAGTTGAAC
AACAATGAATTAAAGATTCTCCGAGCTGACACTTTCTTGGCATAGAGAACTTGGAGTATCTCCAGGCTGACTACAA
TTAATCAAGTATATTGAACGAGGAGCCTTCAATAAGCTCCACAACTGAAAGTTCTCATTCTTAATGACAATCTGA
TTTCATTCTCTTCTGATAATATTTCCGATTGCGCATCTTTGACCCATCTGGATATACGAGGGAACAGAATCCAGAAG
CTCCCTTATATCGGGGTTCTGGAACACATTGGCCGTGTCGTTGAATTGCAACTGGAAGATAACCTTGGAACTGTAG
CTGTGATTTATTGCCCTTAAAGCTTGGCTGGAGAACATGCCATATAACATTTACATAGGAGAAGCTATCTGTGAAA
CTCCAGTGACTTATATGGAAGGCTTTTAAAGAAACCAACAACAAGAGCTATGTCCCATGGGCACCGGCAGTGAT
TTTGACGTGCGCATCTGCCTCCATCTCAGCTGGAATGGCTACACCACTCCCAATGGTCACTACCCAAACATC
TTTACACAGATTAGTAACCTAAACCACCAAAAACAACAATCCTTCCAAGATCTCTGGAATCGTTGCAGGCAAGCCC
TCTCCAACCGCAATCTCAGTCAGATTGTGTCTTACCAAAACAAGGGTGCCTCCTCTAACACCTTGCCCGCACCTTGC
TTCTGCAAAACACACCCCTTCAAGTTGGGACTAAGTGTGAAGTGCCTAAGAGAAAAATATACAGTCTATGTCTGAAGT
GATACCGAAACCTTTAAATGCGAAGAAGCTGCACGTCAATGGCAATAGCATCAAGGATGTGGACGTATCAGACTTCA
CTGACTTTGAAGGACTGGATTGCTTCATCTAGGCAGCAATCAAATTACAGTGATTAAAGGAGACGTATTTCAAAAT
CTCACTAATTTACGACGGCTATATCTCAATGGCAATCAAATTGAGAGACTCTATCCTGAAATATTTTCAAGTCTTCA
TAACCTGCAGTATCTGTATTTGGAATAACAATTGATTAAAGGAAATCTCAGCAGGCACCTTTGACTCCATGCCAAATT
TGCAGTTACTGTACTTAAACAATAATCTCCTAAAGAGCCTGCCTGTTTACATCTTTTCCGGAGCACCCCTTAGCTAGA
CTGAACCTGAGGAACAACAAATTCATGTACCTGCCTGTGAGTGGGGTCTTGTATCAGTTGCAATCTCTTACACAGAT
TGACTTGGAGGGCAACCCATGGGACTGTACTTGTGACTTGGTGGCATTAAGCTGTGGGTGGAGAAGTTGAGCGACG
GGATTGTTGTGAAAGAACTGAAATGTGAGACGCGCTGTTCAAGTTTGCCAACATTGAACTGAAAGTCCCTCAAAATGAA
ATCTTATGTCCCAAACTTTTAAATAAGCCGTCTGCACCAATTCACAAGCCCTGCACCTGCCATTACATTCACTCTCC
TTTGGGTCCCATTGCAAGTCTCCTGGTGGGCCAGTGCTCTGTCTATTTTAAATCTTAAGTATCTTAGTGGTCTCTCA
TTTTAACGGTGTGTTGTTGCTTTTGCCTTCTGTTTTTGTCTGCGACGCAACAAGAAACCCACAGTGAAGCAGGAA
GGCTGGGGAATCCTGACTGTGGCTCCATGCAGCTGCAGCTAAGGAAGCATGACCACAAAACCAATAAAAAAGATGG
ACTGAGCACAGAAGCTTTCAATCCACAACTATAGAACAGATGAGCAAGAGCCACACTTGTGGCTTGAAGAGTTCAG
AACTGGGTTTCATGTTTTCAGATCCTCCAGGACAGAAAGTTGTTATGAGAAATGTGGCCGACAAAGGAGAAAGATTTA
TTACATGTAGATACAGGAAGAGACTGAGCACAATTGATGAGCTGGATGAATTATTCCCTAGCAGGGATTCCAATGT
GTTTATTCAAGATTTTCTTGAAGCAAAAAGGAGTATAATAGCATAGGTGTGAGTGGCTTTGAGATCCGCTATCCAG
AAAAACAACGACAAAAAAGTAAGAAAGTCACTGATAGGTGGCAACCACAGTAAATTTGTTGTGGAACAAAGGAAG
AGTGAGTATTTTGAAGTGAAGGCGAAACTGCAGAGTTCCCTGACTACCTACAGGTCTTGGAGGACAAACAGCTTT
GAACAAGATCTAG

```

An open reading frame (ORF) for MOL2 was identified from nucleotides 1 to 2628. The disclosed MOL2 polypeptide (SEQ ID NO:6) encoded by SEQ ID NO:5 has 876 amino acid residues and is presented using the one-letter code in Table 2B. The SignalP, Psort and Hydropathy profile of MOL2 indicate that this sequence does have a signal peptide localized between amino acids 57 and 58 (TNA-DS) and is likely to be localized to the plasma membrane (0.4600 certainty). Therefore it is likely that MOL2 is available at the appropriate sub-cellular localization and hence accessible for the therapeutic uses described in this application.

Table 2B. Encoded MOL2 protein sequence (SEQ ID NO:6).

```

MIYIQVIFQVMTIEKMFSPFYFLDYFSLFRSIQLFADCKKMFLLWFLIISALISSTNADSDISVEICNVCSVSVENV
LYVNCEKVSRYRPNQLKPPWSNFYHLNFOQNNFLNLIYPNTFLNFSHAVSLHLGNNKLQNIIEGGAFLGLSALKQLHLN
NNEKILRADTFLGIENLEYLQADYNLIKYIERGAFNKLHKLKVLILNDNLISFLPDNIFRFASLTHLDIRGNRIQK
LPYIGVLEHIGRVVELQLEDNPNWNCSDLLPLKAWLENMPYNIYIGEAI CETPSDLYGRLLKETNKQELCPMGTGSD
FDVRIILPPSQLENGYTTPNGHTTQTSLHRLVTKPKTTNPSKISGIVAGKALSNNLSQIVSYQTRVPEPLTPCPAPC
FCKTHPSDLGLSVNCQEKNIQSMSELI PKPLNAKKLHVNGNSIKDVDVSDFTDFEGLDLLHLGNSNQITVIKGDVFHN
LTNLRRLYLNGNQIERLYPEIFSGLHNLQVLYLEYNLIKEISAGTFDSMPNLQLLYLNNLLKSLPVYIFSGAPLAR
LNLRRNKFMYLPVSGVLDQLQSLTQIDLEGPNWDCTCDLVALKLWVEKLSDGIVVKELKCEPVPQFANIELKSLKNE
ILCPKLLNKPSAPFTSPAPAITFTTPLGPISPPGGFVPLSILILSILVVLILTTFVAFCLLVFVLRNKKPTVKHE
GLGNPDCCGSMQLQRLKHDHKTNKIOGLSTEAFIPQTEQMSKSHTCGLKESETGFMFSDPPGQKVVMRNVDKEKDL
LHVDTRKRLSTIDELDFPSRDSNVFIQNFLESKKEYNSIGVSGFEIRYPEKQPDKKSKSLIGGNHSKIIVEQRK
SEYFELKAKIQSSPDYLVLEEQTALNKI

```

The MOL2 nucleic acid sequence, localized on the q26.3-28 region of the X chromosome, has 532 of 854 bases (62%) identical to a *Homo sapiens* Insulin-like growth factor binding protein-like protein mRNA (GENBANK-ID:AB020655|acc:AB020655).

- 5 The full amino acid sequence of the protein of the invention was found to have 318 of 672 amino acid residues (47%) identical to, and 445 of 672 residues (66%) similar to, the 977 amino acid residue Insulin-like growth factor binding protein-like protein from *Homo sapiens* (SPTREMBL-ACC:O94933).

- 10 MOL2 expression in different tissues was examined through TaqMan as described below in Example 1.

Other BLAST results including the sequences used for ClustalW analysis are presented in Table 2C.

Table 2C. BLAST results for MOL2

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 6691962 emb CAB65788.1 (AL080239)	bg256022.1 (similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit)) [Homo sapiens]	853	853/853 (100%)	853/853 (100%)	0.0
gi 14424224 sp O94991 Y918_HUMAN	HYPOTHETICAL PROTEIN KIAA0918 [Homo Sapiens]	966	347/699 (49%)	470/699 (66%)	1 e-173
gi 11877257 emb CAC18888.1 (AL109653)	bg115M3.1 (novel protein) [Homo sapiens]	845	372/868 (42%)	516/868 (58%)	1 e-172

gi 12733935 ref XP_011654.1	KIAA0848 protein [Homo sapiens]	977	313/675 (46%)	438/675 (64%)	e-150
gi 7662336 ref NP_055741.1	KIAA0848 protein [Homo sapiens]	977	313/675 (46%)	438/675 (64%)	e-150

This information is presented graphically in the multiple sequence alignment given in Table 2D (with MOL2 being shown on line 1) as a ClustalW analysis comparing MOL2 with related protein sequences.

Table 2D. Information for the ClustalW proteins:

- 1) Novel MOL2 (SEQ ID NO:6)
- 2) gi|6691962|emb|CAB65788.1| (AL080239) insulin-like growth factor binding protein, acid labile subunit)) [Homo sapiens] (SEQ ID NO:30)
- 3) gi|14424224|sp|O94991|Y918_HUMAN HYPOTHETICAL PROTEIN KIAA0918 [Homo Sapiens] (SEQ ID NO:31)
- 4) gi|11877257|emb|CAC18888.1| (AL109653) bg115M3.1 (novel protein) [Homo sapiens] (SEQ ID NO:32)
- 5) gi|12733935|ref|XP_011654.1| KIAA0848 protein [Homo sapiens] (SEQ ID NO:33)
- 6) gi|7662336|ref|NP_055741.1| KIAA0848 protein [Homo sapiens] (SEQ ID NO:34)

	10	20	30	40	50
MOL2	MIYIQVIFQVMTIEKMF	SYFLDYPSLFRSIQLFADCK	KMFLMFLPLISA		
gi 6691962	-----	YFSLFRSIQLFADCK	KMFLMFLPLISA		
gi 14424224	-----	RRGAQGGKMHTCCPFV	TLQDLHKMHSMTOTLAF		
gi 11877257	-----	MLSGVFFLSVLTIV			
gi 14017925	-----	HRRCLKMLSCVFFLSVLTIV			
gi 12733935	-----	MKPSIAEMLHGRGMFLITISHI			
	60	70	80	90	100
MOL2	LTS-----	STNADSDIISVEICN	-VCSQVSVENVLYNCEKVS	VYRPNQIE	
gi 6691962	LTS-----	STNADSDIISVEICN	-VCSQVSVENVLYNCEKVS	VYRPNQIE	
gi 14424224	SVTSLV-	ISCAETIIYGEICDNAC	PCEKGGILIVSCENRC	IIISIS	
gi 11877257	AG-----	TLQTESRRTAKDICKIR	CLCEKENVNLNCEKGF	TIIVSLIC	
gi 14017925	AG-----	TLQTESRRTAKDICKIR	CLCEKENVNLNCEKGF	TIIVSLIC	
gi 12733935	ALGWITTP	PLIEOSEIDEPCFDF	CVCEVKEGILFHIC	CEKGFNMISQIT	
	110	120	130	140	150
MOL2	PPWSNF	PHLNFNQNFENILYP	NTEENFSAVSLHLGNN	KLQNTIEG	CAFLG
gi 6691962	PPWSNF	PHLNFNQNFENILYP	NTEENFSAVSLHLGNN	KLQNTIEG	CAFLG
gi 14424224	PPRPPI	PHLLSGNLELRNLYP	NEFVQYTGASILHLG	SNVIGDIE	TCAPFG
gi 11877257	PPQYRI	YOLFNGNLLIRLYP	NEFVNVYNAVALHLG	NNGLQETIR	TCAPSG
gi 14017925	PPQYRI	YOLFNGNLLIRLYP	NEFVNVYNAVALHLG	NNGLQETIR	TCAPSG
gi 12733935	EFWSRP	PKLYLDRNSMRKLY	INSEILHLANAVSIN	LGNNALQDIT	TCAPNG
	160	170	180	190	200
MOL2	LSALKQLHLNNNE	KLRLRADTFLGLEN	LEYLQADYNLIK	YTERGAF	NKLE
gi 6691962	LSALKQLHLNNNE	KLRLRADTFLGLEN	LEYLQADYNLIK	YTERGAF	NKLE
gi 14424224	LRGLERLHLNNN	KLRLRADTFLGLEN	LEYLQADYNLIK	YTERGAF	NKLE
gi 11877257	LKTLKRLHLNNN	KLRLRADTFLGLEN	LEYLQADYNLIK	YTERGAF	NKLE
gi 14017925	LKTLKRLHLNNN	KLRLRADTFLGLEN	LEYLQADYNLIK	YTERGAF	NKLE
gi 12733935	LKTLKRLHLNNN	KLRLRADTFLGLEN	LEYLQADYNLIK	YTERGAF	NKLE
	210	220	230	240	250
MOL2	KLKVLILNDNL	ISFLPDNIFRFASL	THLDLRGNRIQL	PYIGVLE	HIGR
gi 6691962	KLKVLILNDNL	ISFLPDNIFRFASL	THLDLRGNRIQL	PYIGVLE	HIGR
gi 14424224	LLQVLILNDNL	ISFLPDNIFRFASL	THLDLRGNRIQL	PYIGVLE	HIGR
gi 11877257	KLKVLILNDNL	ISFLPDNIFRFASL	THLDLRGNRIQL	PYIGVLE	HIGR
gi 14017925	KLKVLILNDNL	ISFLPDNIFRFASL	THLDLRGNRIQL	PYIGVLE	HIGR

gi|12733935| KLRVLLNDNLIPMLPTNLKAVSLTHLDRGNRLKVLGYRGMLOHICRS

260 270 280 290 300

MOL2 VVELQLEENPNWNCSCDLLPLKAWLNNMPPNLYIGBATCETPSDLYGRLUK
gi|6691962| VVELQLEENPNWNCSCDLLPLKAWLNNMPPNLYIGBATCETPSDLYGRLUK
gi|14424224| VVELQLEENPNWNCSCDLLPLKAWLNNMPPNLYIGBATCETPSDLYGRLUK
gi|11877257| VVELQLEENPNWNCSCDLLPLKAWLNNMPPNLYIGBATCETPSDLYGRLUK
gi|14017925| VVELQLEENPNWNCSCDLLPLKAWLNNMPPNLYIGBATCETPSDLYGRLUK
gi|12733935| VVELQLEENPNWNCSCDLLPLKAWLNNMPPNLYIGBATCETPSDLYGRLUK

310 320 330 340 350

MOL2 EITNKQELCPMGITGSDFFVRLILPESQLENGVITP---NGHTH-----Q
gi|6691962| EITNKQELCPMGITGSDFFVRLILPESQLENGVITP---NGHTH-----Q
gi|14424224| EITNKQELCPMGITGSDFFVRLILPESQLENGVITP---NGHTH-----Q
gi|11877257| EITNKQELCPMGITGSDFFVRLILPESQLENGVITP---NGHTH-----Q
gi|14017925| EITNKQELCPMGITGSDFFVRLILPESQLENGVITP---NGHTH-----Q
gi|12733935| EITNKQELCPMGITGSDFFVRLILPESQLENGVITP---NGHTH-----Q

360 370 380 390 400

MOL2 TSLHRLVIRKPKTTNPSKISGLV-AGKALS-NENLSQIVSYQTRVPEPLTP
gi|6691962| TSLHRLVIRKPKTTNPSKISGLV-AGKALS-NENLSQIVSYQTRVPEPLTP
gi|14424224| TSLHRLVIRKPKTTNPSKISGLV-AGKALS-NENLSQIVSYQTRVPEPLTP
gi|11877257| TSLHRLVIRKPKTTNPSKISGLV-AGKALS-NENLSQIVSYQTRVPEPLTP
gi|14017925| TSLHRLVIRKPKTTNPSKISGLV-AGKALS-NENLSQIVSYQTRVPEPLTP
gi|12733935| TSLHRLVIRKPKTTNPSKISGLV-AGKALS-NENLSQIVSYQTRVPEPLTP

410 420 430 440 450

MOL2 CPAPDFKTHPSDLGLSVNCOEKNIQSMSELTPEKLNKAKKLHVNCHSTED
gi|6691962| CPAPDFKTHPSDLGLSVNCOEKNIQSMSELTPEKLNKAKKLHVNCHSTED
gi|14424224| CPAPDFKTHPSDLGLSVNCOEKNIQSMSELTPEKLNKAKKLHVNCHSTED
gi|11877257| CPAPDFKTHPSDLGLSVNCOEKNIQSMSELTPEKLNKAKKLHVNCHSTED
gi|14017925| CPAPDFKTHPSDLGLSVNCOEKNIQSMSELTPEKLNKAKKLHVNCHSTED
gi|12733935| CPAPDFKTHPSDLGLSVNCOEKNIQSMSELTPEKLNKAKKLHVNCHSTED

460 470 480 490 500

MOL2 VDVSEFTDFEGLDLLHLGNNRIAVIQCAFNLTSRRRLYLNGMYLFIY
gi|6691962| VDVSEFTDFEGLDLLHLGNNRIAVIQCAFNLTSRRRLYLNGMYLFIY
gi|14424224| VDVSEFTDFEGLDLLHLGNNRIAVIQCAFNLTSRRRLYLNGMYLFIY
gi|11877257| VDVSEFTDFEGLDLLHLGNNRIAVIQCAFNLTSRRRLYLNGMYLFIY
gi|14017925| VDVSEFTDFEGLDLLHLGNNRIAVIQCAFNLTSRRRLYLNGMYLFIY
gi|12733935| VDVSEFTDFEGLDLLHLGNNRIAVIQCAFNLTSRRRLYLNGMYLFIY

510 520 530 540 550

MOL2 PSMEDGLQSLQVLYLEYVNIKEISAGTFDSMPNLQQLFLNHNLLKSLFVY
gi|6691962| PSMEDGLQSLQVLYLEYVNIKEISAGTFDSMPNLQQLFLNHNLLKSLFVY
gi|14424224| PSMEDGLQSLQVLYLEYVNIKEISAGTFDSMPNLQQLFLNHNLLKSLFVY
gi|11877257| PSMEDGLQSLQVLYLEYVNIKEISAGTFDSMPNLQQLFLNHNLLKSLFVY
gi|14017925| PSMEDGLQSLQVLYLEYVNIKEISAGTFDSMPNLQQLFLNHNLLKSLFVY
gi|12733935| PSMEDGLQSLQVLYLEYVNIKEISAGTFDSMPNLQQLFLNHNLLKSLFVY

560 570 580 590 600

MOL2 IFSSAPLARLNLRNNKEMVLPVSGVLDQLOSTIQIDLEGPNWDCTCDIWA
gi|6691962| IFSSAPLARLNLRNNKEMVLPVSGVLDQLOSTIQIDLEGPNWDCTCDIWA
gi|14424224| IFSSAPLARLNLRNNKEMVLPVSGVLDQLOSTIQIDLEGPNWDCTCDIWA
gi|11877257| IFSSAPLARLNLRNNKEMVLPVSGVLDQLOSTIQIDLEGPNWDCTCDIWA
gi|14017925| IFSSAPLARLNLRNNKEMVLPVSGVLDQLOSTIQIDLEGPNWDCTCDIWA
gi|12733935| IFSSAPLARLNLRNNKEMVLPVSGVLDQLOSTIQIDLEGPNWDCTCDIWA

610 620 630 640 650

MOL2 LKLAWEKISDGVTVKELKCEFPVDFANIELKSLKNNILCEKLLKXPSAP
gi|6691962| LKLAWEKISDGVTVKELKCEFPVDFANIELKSLKNNILCEKLLKXPSAP
gi|14424224| LKLAWEKISDGVTVKELKCEFPVDFANIELKSLKNNILCEKLLKXPSAP
gi|11877257| LKLAWEKISDGVTVKELKCEFPVDFANIELKSLKNNILCEKLLKXPSAP
gi|14017925| LKLAWEKISDGVTVKELKCEFPVDFANIELKSLKNNILCEKLLKXPSAP
gi|12733935| LKLAWEKISDGVTVKELKCEFPVDFANIELKSLKNNILCEKLLKXPSAP

660 670 680 690 700

MOL2 FTSPAPALTFTPLGPIRSPPGS---FVPLSTILSILVV
gi|6691962| FTSPAPALTFTPLGPIRSPPGS---FVPLSTILSILVV

gi 14424224	TPSSIQVPARTSAVT	PAVRLNSTGAPASLGAGCGASSVPLSVLILSLLEV
gi 11877257	-----VLSMNHNTDTERSLSVSPSSYPELHT-----	EVPLSVLILGLLVV
gi 14017925	-----ESPAQPGDSHLTGAPTASAEVEYFSPFG-----	EVPLSVLILSLLVV
gi 12733935	-----	-----
	710 720 730 740 750	
MOL2
gi 6691962	LIILVVFVAFCLLVEVLERN-KKPTVKHIEGLNPDCCSMQOLRKHD	LIILVVFVAFCLLVEVLERN-KKPTVKHIEGLNPDCCSMQOLRKHD
gi 14424224	FILSVFVAGLFVILVLRER-KKNQSDHTSTNNSDVSSFNQCYSVGGGGG	FILSVFVAGLFVILVLRER-KKNQSDHTSTNNSDVSSFNQCYSVGGGGG
gi 11877257	FILSVCFGAGLFVILVLRER-KGVPSVPRNTINLLDVSSFOICYGSSN	FILSVCFGAGLFVILVLRER-KGVPSVPRNTINLLDVSSFOICYGSSN
gi 14017925	-----	-----
gi 12733935	FFSAVFVAGLFVILVLRERKKLPFRSKROEGVDLTGIONQCHRLFEDGG	FFSAVFVAGLFVILVLRERKKLPFRSKROEGVDLTGIONQCHRLFEDGG
	760 770 780 790 800	
MOL2
gi 6691962	-----HRTNKK-----DGLSTEARLPQTEQMSKSHTCGLRESST	-----HRTNKK-----DGLSTEARLPQTEQMSKSHTCGLRESST
gi 14424224	TGGHPHAHVHRRGPALPKVKTTPAGHVYETIPHEPGLHCKNPIYRSREGNS	TGGHPHAHVHRRGPALPKVKTTPAGHVYETIPHEPGLHCKNPIYRSREGNS
gi 11877257	-----TETFDK-----TDGHVYNILPPEVGMCONPIYMOKEGDP	-----TETFDK-----TDGHVYNILPPEVGMCONPIYMOKEGDP
gi 14017925	-----	-----
gi 12733935	GGGGGSGGGGRPTLSSPEKAPPVGHVYETIPHEVTDCCNPIYKPEEE	GGGGGSGGGGRPTLSSPEKAPPVGHVYETIPHEVTDCCNPIYKPEEE
	810 820 830 840 850	
MOL2
gi 6691962	GFMESDPPGQKVVMR-----N--PADKER-DLLHVDI	GFMESDPPGQKVVMR-----N--PADKER-DLLHVDI
gi 14424224	VEDYKOLHELKVITYSS-----NHHLOOQOQPPPPQOQPPPPQLO	VEDYKOLHELKVITYSS-----NHHLOOQOQPPPPQOQPPPPQLO
gi 11877257	VAYGRNLQEFYSYN-----LEEKKEPATP-----	VAYGRNLQEFYSYN-----LEEKKEPATP-----
gi 14017925	-----	-----
gi 12733935	VAVSSAQEAGSAERGGPGTQPPGMGEALGSGQFASTPKENHSNYRTILLE	VAVSSAQEAGSAERGGPGTQPPGMGEALGSGQFASTPKENHSNYRTILLE
	860 870 880 890 900	
MOL2
gi 6691962	-----RKRLSTLDELDELFP-SRDSNVFTON-----	-----RKRLSTLDELDELFP-SRDSNVFTON-----
gi 14424224	LQPGEEERRESHHLRSPAYSSTLSPREDLLSPVQADRFYEG	LQPGEEERRESHHLRSPAYSSTLSPREDLLSPVQADRFYEG
gi 11877257	-----AYTLSATLLELKOAT-PRPELLYCN-----	-----AYTLSATLLELKOAT-PRPELLYCN-----
gi 14017925	-----	-----
gi 12733935	-----KEKEWALAVSSQLNTHTVVAHHHPHPHVAVGVSQVGGTGGDLG	-----KEKEWALAVSSQLNTHTVVAHHHPHPHVAVGVSQVGGTGGDLG
	910 920 930 940 950	
MOL2
gi 6691962	-----FLESKREYNS-----IGVSGFEIRYPER	-----FLESKREYNS-----IGVSGFEIRYPER
gi 14424224	-----FLESKREYNS-----IGVSGFEIRYPER	-----FLESKREYNS-----IGVSGFEIRYPER
gi 11877257	-----ILEPDHCSITPAGNSLPEYKPKPCSPAAYTESPNMDL	-----ILEPDHCSITPAGNSLPEYKPKPCSPAAYTESPNMDL
gi 14017925	-----IAERVRELPS--AG--LVHYN--FCTLPKROFAPSFESE	-----IAERVRELPS--AG--LVHYN--FCTLPKROFAPSFESE
gi 12733935	FRHHEKNGGVVLFPPGGGCGSGSMILDRERPQPAPCTVGFVDCLYGTVER	FRHHEKNGGVVLFPPGGGCGSGSMILDRERPQPAPCTVGFVDCLYGTVER
	960 970 980 990 1000	
MOL2
gi 6691962	OPDR-----KSKKSLGGNHSKIVVQR-KSEPFELKAR	OPDR-----KSKKSLGGNHSKIVVQR-KSEPFELKAR
gi 14424224	OPDR-----KSKKSLGGNHSKIVVQR-KSEPFELKAR	OPDR-----KSKKSLGGNHSKIVVQR-KSEPFELKAR
gi 11877257	RPHQYLHPG-----AGDSLRREVLVYSPPSAVFVFPN-KNEVLEIKAR	RPHQYLHPG-----AGDSLRREVLVYSPPSAVFVFPN-KNEVLEIKAR
gi 14017925	RONQ-----DRINKEVLYGTPRKCFVQS-KPNHPILLQAK	RONQ-----DRINKEVLYGTPRKCFVQS-KPNHPILLQAK
gi 12733935	LKELHVHPGMQYPDLOQDARLKRTLLFSAGKGFTDHTQASDVLEIKAR	LKELHVHPGMQYPDLOQDARLKRTLLFSAGKGFTDHTQASDVLEIKAR
	1010 1020	
MOL2
gi 6691962	LOSSPDYLCVLEEQTALNKI	LOSSPDYLCVLEEQTALNKI
gi 14424224	LOSSPDYLCVLEEQTALNKI	LOSSPDYLCVLEEQTALNKI
gi 11877257	LNVEPDYLCVLEEQTITFQF	LNVEPDYLCVLEEQTITFQF
gi 14017925	PQSEPDYLCVLEEQTATBQL	PQSEPDYLCVLEEQTATBQL
gi 12733935	LQNKPDYLCVLEEQITVRF--	LQNKPDYLCVLEEQITVRF--

Table 2E lists the domain description from DOMAIN analysis results against MOL2. The region from amino acid residue 252 through 302 (SEQ ID NO:6) most probably ($E = 1e^{-6}$) contains a "leucine rich repeat C-terminal" domain, aligned here in Table 2E. This indicates

that the MOL2 sequence has properties similar to those of other proteins known to contain this domain.

Table 2E. Domain Analysis of MOL2

gnl|Smart|smart00082 LRRCT, Leucine rich repeat C-terminal domain
CD-Length = 51 residues, 100.0% aligned
Score = 48.9 bits (115), Expect = 1e-06

		10	20	30	40	50
5	MOL2	NEWNGSCDLPKAWLEN	MPYNIYIG	EAICETESDL		
	Smart smart00082	NEFIICCELRWLRLEA	NRRLQDPV	ILRCASEESL		
		60				
10	MOL2	Y-CRITKETN	KQELCF			
	Smart smart00082	R-CPILLLLP	SSFKCF	(SEQ ID NO:89)		

Chromosomal information

The Insulin-like growth factor binding protein-like protein disclosed in this invention
15 maps to chromosome Xq26.3-28.

Tissue expression

MOL2 is expressed in at least the following tissues: adrenal gland, lymphatic tissues,
and heart. Other tissues known to express insulin-like growth factor binding proteins are
20 likely.

Uses of the Compositions of the Invention

The expression pattern, map location and protein similarity information for MOL2
suggest that this a Insulin-like growth factor binding protein-like protein may function as a
25 member of the Insulin-like growth factor binding protein-like protein family. Therefore, the
MOL2 nucleic acids and proteins are useful in potential therapeutic applications implicated,
for example but not limited to, in various pathologies /disorders as described below and/or
other pathologies/disorders. Potential therapeutic uses for MOL2 are, for example but not
limited to, the following: (i) Protein therapeutic, (ii) small molecule drug target, (iii) antibody
30 target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) diagnostic and/or
prognostic marker, (v) gene therapy (gene delivery/gene ablation), (vi) research tools, and
(vii) tissue regeneration *in vitro* and *in vivo* (regeneration for all these tissues and cell types
composing these tissues and cell types derived from these tissues).

The MOL2 nucleic acids and proteins are useful in potential therapeutic applications
35 implicated in various diseases and disorders described below and/or other pathologies and
disorders. For example, but not limited to, a cDNA encoding the a Insulin-like growth factor
binding protein-like protein may be useful in gene therapy, and the a Insulin-like growth factor

binding protein-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from cancer, diabetes, cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD),

5 atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, graft versus host disease (GVHD), lymphoedema, adrenoleukodystrophy, and/or congenital adrenal hyperplasia. MOL2, or

10 fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

These materials are further useful in the generation of antibodies that bind immuno-specifically to the novel MOL2 substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from

15 hydrophobicity charts, as described in the "Anti-MOLX Antibodies" section below. The disclosed MOL2 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated MOL2 epitope is from about amino acids 75 to 120. In another embodiment, a MOL2 epitope is from about amino acids 180 to 200. In additional embodiments, MOL2 epitopes are from about amino acids 280 to 380, 400 to 450,

20 475 to 500, and from about amino acids 680 to 850. These novel proteins can also be used to develop assay systems for functional analysis.

MOL3

MOL3a

25 An additional protein of the invention, referred to herein as MOL3a, is a human Semaphorin B-like protein. The novel nucleic acid of 2271 nucleotides (SC85516573_EXT, SEQ ID NO:7) encoding a novel olfactory receptor-like protein is shown in Table 3A. An open reading frame (ORF) was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TAA codon at nucleotides 2269-2271. The nucleotide

30 sequence is presented in Table 3A with the start and stop codons are in bold letters.

Table 3A. MOL3a Nucleotide Sequence (SEQ ID NO:7)

ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCCTTTCTCTTCCA ACTGCTTC AGCTGCTGCTGCCGACGACGACCGCGGGGGAGCGGGCAGGGGCCCATGCCAGGGTCAGATACTA
--

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TGCAGGGGATGAACGTAGGGCACCTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTG
CTCCTGAGTGGTGTATGGAATACCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCC
AGGATCCAGGGGTCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGA
ATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTCCTTAC
AATGTCACCCATCTCTACACCTGCGGCACCTTCGCCCTCAGCCCTGCTTGTACCTTCATTGAACCTC
AAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCCTTGA
CCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACCTTC
CTGGGCAGTGAGCCCATCTGTATGCGCACACTGGGATCCCAGCCTGTCTCAAGACCGACAACCTTCC
TCCGCTGGCTGCATCATGACGCCCTCTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTT
CTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGTGGCTAGAGTC
TGCAAGAATGACGTGGGCGGGGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCTGAAGGCCCAGC
TGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCGGCCGA
TTCTCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCAGTGGCAGGTTGGCGGGACCCAGGAGC
TCTGCGGTTTGTGCTTCTCTCTCTTGGACATTGAACGTGCTTTAAGGGGAAATACAAAGAGTTGA
ACAAAGAACTTCAAGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTC
AGTGGGCCCCCTCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCTGATGGATGAGCAAGTG
GTGGGGAGCCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCACGG
GCCTTGATGGGCACAGCCATCTTGTCTATGTAAGTGGGAACCAAGTACAGGGTCGCTCCACAAGGCTGT
GGTAAGTGGGGACAGCAGTGTCTCATCTGGTGGAGAGATTGAGTGTTCCTGACCCCTGAACCTGTT
CGCAACCTGCAGCTGGCCCCCAGCCAGGTCAGTGTGTTGAGGCTTCTCAGGAGGTGTCTGGAGGG
TGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCCACTG
TGCTTGGGACCCCTGAGTCCCGACTCTGCTCTCTTAGGAACCTCCTGGAAGCAGGACATGGAGCGGGGG
AACCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAA
TCGTTAAAGAAGTCTGGCTGTCCCCAACTCCATCTGGAGCTCCCCTGCCCCACCTGTGACCCCTT
GGCTCTTATTATTGGAGTCAATGGCCAGCAGCAGTCCAGAAAGCCTCTTCCACTGTCTACAATGGC
TCCCTCTTGGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAAGTGTGGGCAACTGAGAATGGCT
TTTCACTCCCTGTGATCTCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCTCTGAAC
GGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCT
GCCCAGCAGTCTACTGGCCCCACTTTGTCACTGTCACTGTCTCTTTCCTTAGTGCTTTTCAGGAG
CCCTCATCATCTCGTGGCTCCCATGAGAGCACTCCGGGCTCGGGCAAGGTTACAGGGCTGTGA
GACCTTGGCCCTTGGGAGAAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGC
AGGACCTCTGCCAGTGTGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAA

```

The disclosed MOL3a polypeptide (SEQ ID NO:8) encoded by SEQ ID NO:7 has 756 amino acid residues, and is presented using the one-letter code in Table 3B. The MOL3a protein was analyzed for signal peptide prediction and cellular localization. SignalP results predict that MOL3a is cleaved between position 31 and 32 (TTA-GG) of SEQ ID NO:8. Psort and Hydropathy profiles also predict that MOL3a is likely to be localized at the plasma membrane (certainty of 0.7300).

Table 3B. Encoded MOL3a protein sequence (SEQ ID NO:8).

```

MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGMFPRVRYAGDERRALSFFHQKGLQDFDTLLSGDGNT
LYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQCFNPIRVLVSYNVTHLYTCGTFAPSPA
CTFIELQDSYLLPISBDKVMGKQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLR
WLHHDASFVAAPSTQVYFFFEETASEFDFFERLHSTRVARVCKNDVGGEKLLQKKNTTFLKAQLLCTQPGQLP
FNVI RHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPR
PGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTSGLSHKAVVSG
DSSAHLVEBILFPDPPEPVRNLQAPLQGAFFVFGSGGVWRVPRANCSEVSCVDCVLARDPHCAWDPE SRLCSL
RNSWKQDMERGNPEWACASGPMRSRLRPQSRPQIVKEVLAVPNSILELPCPHLSALASYWHSHPAAVPBASSTV
YNGSLLLIVQDGVGGLYQCWATENGFSYPVISYVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQSY
WPHFVTVTVLFAVLVSGALIIIVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVEDADNNC
LGTEVA

```

The MOL3a nucleic acid sequence has 1398/1672 (83%) identical to a mouse Semaphorin B mRNA (GENBANK-ID: X85991).

The full amino acid sequence of MOL3a was found to have 628 of 760 (82%) identical to, 674 of 760 residues (88%) homologous with, the 760 amino acid residue Semaphorin B protein from mouse (ptrn: SWISSNEW-ACC:Q62178).

5 MOL3a expression in different tissues was examined through TaqMan as described below in Example 1.

MOL3a also has high homology to the proteins disclosed in the BLASTP searches of the proprietary PATP database shown in Table 3C.

Table 3C. BLAST results for MOL3a					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
patp:AAB24084	Human PRO1317 protein	761	751/761 (98%)	753/761 (98%)	0.0
patp:AAY99418	Human PRO1317 (UNQ783)	761	751/761 (98%)	753/761 (98%)	0.0
patp:AAB66043	Human TANGO 265	761	751/761 (98%)	753/761 (98%)	0.0
patp:AAB66167	Unidentified	761	751/761 (98%)	753/761 (98%)	0.0
patp:AAB37984	Human secreted protein encoded by gene 1 clone HTDAA93	762	743/761 (97%)	745/761 (97%)	0.0
patp:AAB66045	Human TANGO 265 mature protein	730	720/730 (98%)	722/730 (98%)	0.0
patp:AAB66046	Human TANGO 265 extracellular domain	652	642/652 (98%)	644/652 (98%)	0.0

Tissue Localization

10 MOL3a is expressed in at least the following tissues: Pituitary Gland, Thalamus

Chromosomal Localization

MOL3a maps to chromosome 1.

MOL3b

In the present invention, the target sequence identified previously, MOL3a, was subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on *in silico* predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences sequences from other species. These primers were then employed in

PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus. Usually the resulting amplicons were gel purified, cloned and sequenced to high redundancy. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported below, which is designated MOL3b, or alternatively Accession Number CG53027-02. This is a spliced variant of the previously identified sequence (Accession Number SC85516573_EXT) at amino acids 293-329.

A protein of the invention, referred to herein as MOL3b, is a human Semaphorin B-like protein. The novel nucleic acid of 2281 nucleotides (CG53027-02, SEQ ID NO:9) encoding a Semaphorin B-like protein is shown in Table 3D. An open reading frame (ORF) was identified beginning with a non-initiating codon for the mature protein at nucleotides 2-4 and ending with non-stop codon at nucleotides 2264-2266. The open reading frame may be extendable in both the 5' and 3' directions because of the lack of traditional start and stop codons. The nucleotide sequence is presented in Table 3D with the start and stop codons in bold letters and the 5' and 3' untranslated regions underlined.

Table 3D. MOL3b Nucleotide Sequence (SEQ ID NO:9)

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GCCTGTGCTAGAGTTTAAGCTACCTCAGTGCCTAGGCAGTTGTTGTCAGCGTCCACATCACTGGCAGAGGTCCT
GCATTCCTTGGGAGACTGGAGGTGTTGCTCTCTGCTTAACGGGGCCTTCTCCCGAGGGCGCAGGGTCTCACAGCC
CTGAACCTTGCCCGAGCCCGAGTGTCTCTCAATGGGGAGGCCACGAGGATGATGAGGGCTCCTGAAAGCACTAA
GGCAAAGAGGACAGTGACAGTGACAAAGTGGGGCCAGTAGGACTGCTGGGCAGCCAGGGCGGCCCCACCACTGAC
CCTGGTCAACGGGACCTTCACATGCTCCCGGGGATGCCCTGCCAGTTCAGGATCCAGGGCCAGGGTCTGGTCTCTG
GCTGTCCACCCAGTAGGAGATCACAGGGTATGAAAAGCCATTCTCAGTTGCCAGCACTGGTAGAGACCCCCAAC
TCCATCCTGCACTATCAGCAAGAGGGAGCCATTGTAGACAGTGGAAGAGGCTTCTGGGACTGCTGCTGGGCCATG
ACTCCAATAATAAGAGGCCAAGGCTGACAGGTGGGGGACAGGGAGCTCCAGGATGGAGTTGGGGACAGCCAGGAC
TTCTTTAATGATTTCGGGGCGGCTCTGAGGCGGAAGGCTCTGCTCATGGGGCACTGGGCACATGCCCACTCTGG
GTTCCCCCGCTCCATGTCTGCTTCCAGGAGTTCAGGTTGGGGGACAGCAGGAGGCAACAGGTTCCGGGACTCAGG
GTCCCAGGCACAGTGGGGGTCCCGGGCAAGGACACAGTCCACACAGCTCTCATAGACACTACAGTTGGCTCGGGG
CACCCTCCAGACACCTCCTGAGAAGCCTACAAACACTGCACCCCTGGGTGGGGGCCAGCTGCAGGTTGCGAACAGG
TTCAGGTCAGGGAAACAGCTGAATCTCTTCCACCAGATGAGCACTGCTGTCCCACTTACCACAGCCTTGTGGAG
CGACCCTGTGGTGGTTCCAGGTACATGACAAGATGGCTGTGCCCATCAAGGCCCTGGGCTGTCTCCACTGCAAG
CCGTGTATACTCCAGCCAGATTTCACCAGCAGGGGCGTCCCCACCACTTGCTCATCCATCAGGAAATGGTCCTT
CATGAAGGTCAGGGCCTTATCAGAGGAGGGGCCACTGAGCAACTGCCTGGCCGGGGGTTGGTCTCAGGGCCCCCT
ATAAGTAGTCCAGCGTGAAGTTCTTTGTTCAACTCTTTGTATTTCCTTAAAGACACGTTCAATGTCCAAGAG
AGAGAAGGCACAAACCGCAGAGCTCCTGGTCCCAGCAACCTGCCACTGGGAGGTGAAGACTGCGTAGATGTGGGG
AGCTGTGGGAGAATCGGCGGGGAGCAGGACCGCGTGGCGGATGACGTTGAAGGGCAGCTGCCCGGCTGGGTGCA
GAGCAGCTGGGCCTTCAGGAAGGTGGTCCACTTCTTCTGCAGCAGCTTTTCGCCGCCACGTCATTCTGCAGAC

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TCTAGCCACCCGCGATGTGTGGAGCCTCTCAAAGAAGTCAAACCTCGCTGGCTGTCTCCTCGAAGAAGAAGTAGAC
GACCTGGGTGGAAGGATGGCTGCCACAAAGGAGGCGTCATGATGCAGCCAGCGGAGGAAGTTGTCGGTCTTGAG
GACAGGCTGGGATCCAGTGTGCGCATCAGGATGGGCTCACTGCCAGGAAGTTGTTTCATAGTACCAGAAATAGAG
CATCCCATCCACCAAGACAGCGTATGCTTGTGAGCGGGGTCAAAGGGGCTTTGGCCTTTTCCCTCCATGACCTT
GTCTCCGAGATGGGCAACAGGTAGGAATCTTGAAGTTCAATGAAGGTACAAGCAGGGCTGAAGGCGAAGGTGCC
GCAGGTGTAGAGATGGGTGACATTGTAAGAAACCAGGACACGGATGAAGTTGAAACACTGTGTCTCATTTGCTCTT
CTTCTTAAAGGCACATTCACCTCTTTTCTGTCTGCTGGCTGGCCACGGTATCATGTTCTTTAGCCTGGGGACCCC
TGGATCCTGGATATCCAAGGCCAGAATGGCTTCTCGAGCCCCACGTCAGAGAGTATTTCCATCACCACCTCAGGAG
CAGAGTGTCAAATCCTGGAGGCCCTTCTGGTGAAGAAGCTAAGTGCCCTACGTTTCATCCCTGCATAGTATCT
GACCTTGGGCATGGGCCCCTGCCCCCTCCCCCGCGGTCTGTCGTCGGCAGCAGCAGCTGAAGCAGTTGGAAGAG
GAAAAGGCCAGGAGGCTCCAGGGGTCCAGG

```

The disclosed MOL3b polypeptide (SEQ ID NO:10) encoded by SEQ ID NO:9 has 754 amino acid residues, and is presented using the one-letter code in Table 3E. The MOL3b protein was analyzed for signal peptide prediction and cellular localization. SignalP results predict that MOL3b is cleaved between position 24 and 25 (TTA-GG) of SEQ ID NO:10. Psort and Hydropathy profiles also predict that MOL3b is likely to be localized at the plasma membrane (certainty of 0.7300).

Table 3E. Encoded MOL3b protein sequence (SEQ ID NO:10).

```

LDPWSLLGLFLFQLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQDFDLLLLSGDNTLYVGARE
AILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFI RVLVSYNVTHLYTCGTFAFSPACTFIELQ
DSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLTNDNLRWLHHDAS
FVAAPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHA
VLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAPSLLDIERVFKGKYKELNKETSRWTTYRGPEPNRPFGSCSVG
PSSDKALTFMKDHFLMDEQVVGTPLLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTGSLHKAVVSGDSSAHLV
EEIQLFDPPEPVRNLQALPTQGAFFVGFSGGVWRVPRANC SVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLN
SWKQDMERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAPVEASSTVYN
GSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFAVLVSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLG
TEVA

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The MOL3b nucleic acid sequence has 1910 of 2279 bases (83%) identical to a gb:GENBANK-ID:MMRNASEMB|acc:X85991.1 mRNA from *Mus musculus* (*M. musculus* mRNA for semaphorin B).

The full amino acid sequence of the protein of the invention was found to have 722 of 755 amino acid residues (95%) identical to, and 723 of 755 amino acid residues (95%) similar to, the 762 amino acid residue ptmr:TREMBLNEW-ACC:BAB20087 protein from Homo sapiens (Human) (SEMB).

The presence of identifiable domains in the protein disclosed herein was determined by searches versus domain databases such as Pfam, PROSITE, ProDom, Blocks or Prints and then identified by the Interpro domain accession number. Significant domains are summarized in Table 3F.

Table 3F Domain search for MOL3b

HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: pfamHMMs
 Sequence file: /data4/genetools/kspytek35060Cg53027_01ProteinFasta.txt
 Query: CG53027_01

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
Sema	Sema domain	618.4	4.2e-182	1
Plexin_repeat	Plexin repeat	22.0	0.013	1
integrin_B	Integrins, beta chain	6.5	0.063	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
Sema	1/1	57	471 ..	1	490 []	618.4	4.2e-182
integrin_B	1/1	495	509 ..	1	14 [.	6.5	0.063
Plexin_repeat	1/1	489	555 ..	1	67 []	22.0	0.013

Tissue Localization

MOL3b is expressed in at least the following tissues: thalamus and Pituitary Gland.

Expression information was derived from the tissue sources of the sequences that were included in the derivation of the sequence of MOL3b.

Chromosomal Localization

MOL3b maps to chromosome 1. This assignment was made using mapping information associated with genomic clones, public genes and ESTs sharing sequence identity with the disclosed sequence and CuraGen Corporation's Electronic Northern bioinformatic tool.

The disclosed MOL3a protein (SEQ ID NO:8) also has good identity with a number of other proteins, as shown in Table 3G.

Table 3G. BLAST results for MOL3a					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 12248382 dbj B AB20087.1 (AB029394)	SEMB [Homo sapiens]	762	719/762 (94%)	722/762 (94%)	0.0
gi 7305469 ref NP _038686.1	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A [Mus musculus]	760	626/760 (82%)	671/760 (87%)	0.0

gi 11641291 ref NP_071762.1	hypothetical protein FLJ12287 similar to semaphorins [Homo sapiens]	328	318/328 (96%)	320/328 (96%)	0.0
gi 12698035 dbj BAB21836.1 (AB051532)	KIAA1745 protein (Homo sapiens)	893	296/760 (38%)	422/760 (54%)	e-123
gi 8134698 sp Q62179 SM4B_MOUSE	SEMAPHORIN 4B (SEMAPHORIN C) (SEMA C)	782	268/684 (39%)	382/684 (55%)	e-123

This information is presented graphically in the multiple sequence alignment given in Table 3H (with MOL3a being shown on line 1 and MOL3b on line 2) as a ClustalW analysis comparing MOL3 with related protein sequences.

5

Table 3H. Information for the ClustalW proteins:

- 1) MOL3a (SEQ ID NO:8)
- 2) MOL3b (SEQ ID NO:10)
- 3) gi|12248382|dbj|BAB20087.1| (AB029394) SEMB [Homo sapiens] (SEQ ID NO:35)
- 4) gi|7305469|ref|NP_038686.1| sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A [Mus musculus] (SEQ ID NO:36)
- 5) gi|11641291|ref|NP_071762.1| hypothetical protein FLJ12287 similar to semaphorins [Homo sapiens] (SEQ ID NO:37)
- 6) gi|12698035|dbj|BAB21836.1| (AB051532) KIAA1745 protein [Homo sapiens] (SEQ ID NO:38)
- 7) gi|8134698|sp|Q62179|SM4B_MOUSE SEMAPHORIN 4B (SEMAPHORIN C) (SEMA C) (SEQ ID NO:39)

10

15

	10	20	30	40
MOL3a			
MOL3b	----- ----- ----- ----- ----- ----- ----- -----			
gi 12248382	----- ----- ----- ----- ----- ----- ----- -----			
gi 7305469	----- ----- ----- ----- ----- ----- ----- -----			
gi 11641291	----- ----- ----- ----- ----- ----- ----- -----			
gi 12698035	VCQGFLDPVSHLPPPRSGGGGPRGDSGADRGAE LPPVSPA			
gi 8134698	----- ----- ----- ----- ----- ----- ----- -----			
	50	60	70	80
MOL3a	----- ----- ----- ----- ----- ----- ----- -----			
MOL3b	----- ----- ----- ----- ----- ----- ----- -----			
gi 12248382	----- ----- ----- ----- ----- ----- ----- -----			
gi 7305469	----- ----- ----- ----- ----- ----- ----- -----			
gi 11641291	----- ----- ----- ----- ----- ----- ----- -----			
gi 12698035	EPPEPEPRDTVAPALRMLRTAMGLRSWLAAPWGALPPRPP			
gi 8134698	----- ----- ----- ----- ----- ----- ----- -----			
	90	100	110	120
MOL3a			
MOL3b	----- ----- ----- ----- ----- ----- ----- -----			
gi 12248382	----- ----- ----- ----- ----- ----- ----- -----			
gi 7305469	----- ----- ----- ----- ----- ----- ----- -----			
gi 11641291	----- ----- ----- ----- ----- ----- ----- -----			
gi 12698035	LLGLLGLLLQLPPPTWALSPTLSLPLGSEERPFLLRFA			
gi 8134698	----- ----- ----- ----- ----- ----- ----- -----			

	130	140	150	160
MOL3a	KGLQDFD	TLLSGD	NTLYVG	AREAILALDIQDPGVPR-L
MOL3b	KGLQDFD	TLLSGD	NTLYVG	AREAILALDIQDPGVPR-L
gi 12248382	KGLQDFD	TLLSGD	NTLYVG	AREAILALDIQDPGVPR-L
gi 7305469	KGLQDFD	TLLSGD	NTLYVG	AREAILALDIQDPGVPR-L
gi 11641291	KGLQDFD	TLLSGD	NTLYVG	AREAILALDIQDPGVPR-L
gi 12698035	KGLQDFD	TLLSGD	NTLYVG	AREAILALDIQDPGVPR-L
gi 8134698	KGLQDFD	TLLSGD	NTLYVG	AREAILALDIQDPGVPR-L
	170	180	190	200
MOL3a	KNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVT			
MOL3b	KNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVT			
gi 12248382	KNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVT			
gi 7305469	KNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVT			
gi 11641291	KNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVT			
gi 12698035	KNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVT			
gi 8134698	KNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVT			
	210	220	230	240
MOL3a	HLVTCGTFAFSPACTFIELQDSYLLPISEDKVME--GKGQ			
MOL3b	HLVTCGTFAFSPACTFIELQDSYLLPISEDKVME--GKGQ			
gi 12248382	HLVTCGTFAFSPACTFIELQDSYLLPISEDKVME--GKGQ			
gi 7305469	HLVTCGTFAFSPACTFIELQDSYLLPISEDKVME--GKGQ			
gi 11641291	HLVTCGTFAFSPACTFIELQDSYLLPISEDKVME--GKGQ			
gi 12698035	HLVTCGTFAFSPACTFIELQDSYLLPISEDKVME--GKGQ			
gi 8134698	HLVTCGTFAFSPACTFIELQDSYLLPISEDKVME--GKGQ			
	250	260	270	280
MOL3a	SPFDPAHKHTAVLVDCMLYSGTMNFLGSEPILMRTLGSQ			
MOL3b	SPFDPAHKHTAVLVDCMLYSGTMNFLGSEPILMRTLGSQ			
gi 12248382	SPFDPAHKHTAVLVDCMLYSGTMNFLGSEPILMRTLGSQ			
gi 7305469	SPFDPAHKHTAVLVDCMLYSGTMNFLGSEPILMRTLGSQ			
gi 11641291	SPFDPAHKHTAVLVDCMLYSGTMNFLGSEPILMRTLGSQ			
gi 12698035	SPFDPAHKHTAVLVDCMLYSGTMNFLGSEPILMRTLGSQ			
gi 8134698	SPFDPAHKHTAVLVDCMLYSGTMNFLGSEPILMRTLGSQ			
	290	300	310	320
MOL3a	PVLKTDNFLRWLHHDASFVAAIP-----STQVVYFF			
MOL3b	PVLKTDNFLRWLHHDASFVAAIP-----STQVVYFF			
gi 12248382	PVLKTDNFLRWLHHDASFVAAIP-----STQVVYFF			
gi 7305469	PVLKTDNFLRWLHHDASFVAAIP-----STQVVYFF			
gi 11641291	PVLKTDNFLRWLHHDASFVAAIP-----STQVVYFF			
gi 12698035	PVLKTDNFLRWLHHDASFVAAIP-----STQVVYFF			
gi 8134698	PVLKTDNFLRWLHHDASFVAAIP-----STQVVYFF			
	330	340	350	360
MOL3a	FEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTF			
MOL3b	FEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTF			
gi 12248382	FEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTF			
gi 7305469	FEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTF			
gi 11641291	FEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTF			
gi 12698035	FEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTF			
gi 8134698	FEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTF			
	370	380	390	400
MOL3a	LKAQLLCQOP--GQLPFNVIRHAVLLPADSP--TAPPIYAV			
MOL3b	LKAQLLCQOP--GQLPFNVIRHAVLLPADSP--TAPPIYAV			
gi 12248382	LKAQLLCQOP--GQLPFNVIRHAVLLPADSP--TAPPIYAV			
gi 7305469	LKAQLLCQOP--GQLPFNVIRHAVLLPADSP--TAPPIYAV			
gi 11641291	LKAQLLCQOP--GQLPFNVIRHAVLLPADSP--TAPPIYAV			
gi 12698035	LKAQLLCQOP--GQLPFNVIRHAVLLPADSP--TAPPIYAV			
gi 8134698	LKAQLLCQOP--GQLPFNVIRHAVLLPADSP--TAPPIYAV			

	410	420	430	440
MOL3a	FTSQWQVGGTRSSAVCAFSLLDI	ERVFKGKYKELNKETSR		
MOL3b	FTSQWQVGGTRSSAVCAFSLLDI	ERVFKGKYKELNKETSR		
gi 12248382	SPPSGQVGGTRSSAVCAFSLLDI	ERVFKGKYKELNKETSR		
gi 7305469	FTSQWQVGGTRSSAVCAFSLLDI	ERVFKGKYKELNKETSR		
gi 11641291				
gi 12698035	FTSQWHRGTTGSAVCFVETMKD	VCRVFSGLYKEVNRRETQ		
gi 8134698	FTSQWHRGTTGSAVCFVETMKD	VCRVFSGLYKEVNRRETQ		
	450	460	470	480
MOL3a	WTTYRGPETNPRPGSCSVGPS		SDKALTFM	
MOL3b	WTTYRGPETNPRPGSCSVGPS		SDKALTFM	
gi 12248382	WTTYRGPETNPRPGSCSVGPS		SDKALTFM	
gi 7305469	WTTYRGSEVSPRPGSCSMGPS		SDKALTFM	
gi 11641291				
gi 12698035	WYVVTHTDVPDPRPGACITNS	ARERKINSSSLQLPDEVN		
gi 8134698	WYVVTHTDVPDPRPGACITNS	ARERKINSSSLQLPDEVN		
	490	500	510	520
MOL3a	KDHFLMDEQVVGTPLLVKSGVEY	TRLAVETAQGLDGHSHL		
MOL3b	KDHFLMDEQVVGTPLLVKSGVEY	TRLAVETAQGLDGHSHL		
gi 12248382	KDHFLMDEQVVGTPLLVKSGVEY	TRLAVETAQGLDGHSHL		
gi 7305469	KDHFLMDEQVVGTPLLVKSGVEY	TRLAVEFAQGLDGHSHL		
gi 11641291				
gi 12698035	KDHFLMDGQVRSRMLLQPOAR	QVAVHRVPGLIH-ETQD		
gi 8134698	KDHFLMDGQVRSRMLLQPOAR	QVAVHRVPGLIH-STQD		
	530	540	550	560
MOL3a	VMYLGTTGSLHKAVVSGDSSAHL	VEEIQLFDPDPEVRNL		
MOL3b	VMYLGTTGSLHKAVVSGDSSAHL	VEEIQLFDPDPEVRNL		
gi 12248382	VMYLGTTGSLHKAVVSGDSSAHL	VEEIQLFDPDPEVRNL		
gi 7305469	VMYLGTTGSLHKAVVSGDSSAHL	VEEIQLFDPDPEVRNL		
gi 11641291	VMYLGTTGSLHKAVVSGDSSAHL	VEEIQLFDPDPEVRNL		
gi 12698035	VMYLGTTGSLHKAVVSGDSSAHL	VEEIQLFDPDPEVRNL		
gi 8134698	VMYLGTTGSLHKAVVSGDSSAHL	VEEIQLFDPDPEVRNL		
	570	580	590	600
MOL3a	QLAPTQGAFFVGFSGGVWRVPR	ANCSVYESCVDCVLARDP		
MOL3b	QLAPTQGAFFVGFSGGVWRVPR	ANCSVYESCVDCVLARDP		
gi 12248382	QLAPTQGAFFVGFSGGVWRVPR	ANCSVYESCVDCVLARDP		
gi 7305469	QLAPAQGAFFVGFSGGVWRVPR	ANCSVYESCVDCVLARDP		
gi 11641291	QLAPTQGAFFVGFSGGVWRVPR	ANCSVYESCVDCVLARDP		
gi 12698035	LDLTHRGGLYAAASHSGVVOVP	ANCSVYESCVDCVLARDP		
gi 8134698	LDLTHRGGLYAAASHSGVVOVP	ANCSVYESCVDCVLARDP		
	610	620	630	640
MOL3a	HCAWD-PESRLCSLR-----	NSWKQDMERGNPEWACASG		
MOL3b	HCAWD-PESRTCCLLS-APNLNS	WKQDMERGNPEWACASG		
gi 12248382	HCAWD-PESRTCCLLS-APNLNS	WKQDMERGNPEWACASG		
gi 7305469	HCAWD-PESRLCSLLS-G-STK	PKQDMERGNPEWACASG		
gi 11641291	HCAWD-PESRTCCLLS-APNLNS	WKQDMERGNPEWACASG		
gi 12698035	YCAWSSGSSCKHVSLEYQPOL	ATPKTODTEGASAKDTCSAS		
gi 8134698	YCAWSSGSSCKHVSLEYQPOL	ATPKTODTEGASAKDTCSAS		
	650	660	670	680
MOL3a	PMSRSLRPQSRPQIIKEVLAVP	NSILELPCPHLSALASYY		
MOL3b	PMSRSLRPQSRPQIIKEVLAVP	NSILELPCPHLSALASYY		
gi 12248382	PMSRSLRPQSRPQIIKEVLAVP	NSILELPCPHLSALASYY		
gi 7305469	PMSRSLRPQSRPQIIKEVLAVP	NSILELPCPHLSALASYY		
gi 11641291	PMSRSLRPQSRPQIIKEVLAVP	NSILELPCPHLSALASYY		
gi 12698035	SVVSPSFVPTGKPCQVQFQ	PNITVNTLACPLLSNLATRL		

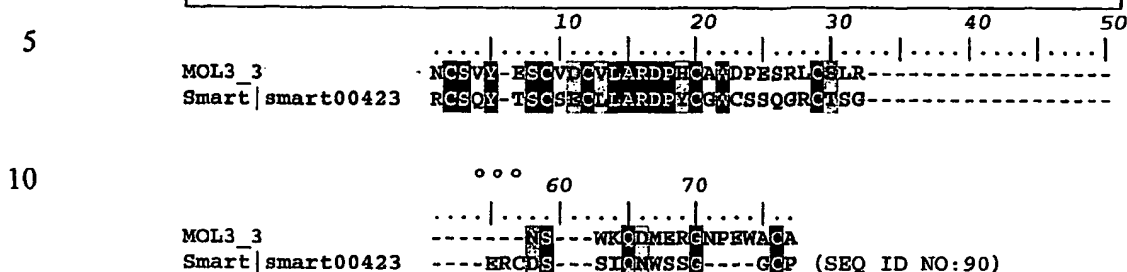
gi 8134698	SYKARFLVPG--KPCCKVQIQPNVNTLACPTLSNLEATRL
690.....700.....710.....720.....
MOL3a	WSHG--PAAVPEASSTVYNGSLLLIQDGVGGLYQCWATE
MOL3b	WSHG--PAAVPEASSTVYNGSLLLIQDGVGGLYQCWATE
gi 12248382	WSHG--PAAVPEASSTVYNGSLLLIQDGVGGLYQCWATE
gi 7305469	WSHG--RAKUISEASTVYNGSLLLIQDGVGGLYQCWATE
gi 11641291	WSHG--PAAVPEASSTVYNGSLLLIQDGVGGLYQCWATE
gi 12698035	WLRNGAPVNASASCHVLPTEGDLILLVGTQQ-LGEKQCWSTLE
gi 8134698	WVNGAPVNASASCRVLPTEGDLILLVGSQQGLGVQCASIE
730.....740.....750.....760.....
MOL3a	NGFSYPVISYWVDSQDC-TLALDPELAGIPREHVKVPLTR
MOL3b	NGFSYPVISYWVDSQDC-TLALDPELAGIPREHVKVPLTR
gi 12248382	NGFSYPVISYWVDSQDC-TLALDPELAGIPREHVKVPLTR
gi 7305469	NGFSYPVISYWVDSQDC-PLALDPELAGIPREHVKVPLTR
gi 11641291	NGFSYPVISYWVDSQDC-TLALDPELAGIPREHVKVPLTR
gi 12698035	EGHQQLVASYCPFVVEDGVADQTEGGSYFVIISTSRVSA
gi 8134698	EGHQQLVASYCPFVMEEGVMDQKNQDCTEVIINTSRVSA
770.....780.....790.....800.....
MOL3a	VSGG-AALAAQOSYNPHFVTVTVLFAVLVSGALIILVASP
MOL3b	VSGG-AALAAQOSYNPHFVTVTVLFAVLVSGALIILVASP
gi 12248382	VSGG-AALAAQOSYNPHFVTVTVLFAVLVSGALIILVASP
gi 7305469	VSGG-ASYAAQOSYNPHFLEVTVLFAVLVSGALIILVASP
gi 11641291	VSGG-AALAAQOSYNPHFVTVTVLFAVLVSGALIILVASP
gi 12698035	PAGGRDSWGADKSYNKEFLVMCTLFVLAIVLLPVLFLFYRH
gi 8134698	PAGGRDSWGADKSYNKEFLVMCTLFVLAIVLLPVLFLFYRH
810.....820.....830.....840.....
MOL3a	LRALRARGKVQGCETLR-----PGEKAPLSREQHLQS
MOL3b	LRALRARGKVQGCETLR-----PGEKAPLSREQHLQS
gi 12248382	LRALRARGKVQGCETLR-----PGEKAPLSREQHLQS
gi 7305469	LGALRARGKVQGCETLR-----PREKAPLSREQHLQS
gi 11641291	LRALRARGKVQGCETLR-----PGEKAPLSREQHLQS
gi 12698035	RNSMKVFLKQGECAVHPKTCPVVLPPETRFLNGLGPPFT
gi 8134698	RDGMNLFLLKQGECAVHPKTRPIVLPPETRFLNGLGPPFT
850.....860.....870.....880.....
MOL3a	PKECRTSASDVDAENN-----
MOL3b	PKECRTSASDVDAENN-----
gi 12248382	PKECRTSASDVDAENN-----
gi 7305469	SKDHRTSASDVDAENN-----
gi 11641291	PKECRTSASDVDAENN-----
gi 12698035	PLDHRGYQSLSDSPPGSRVFTSEKRPLSIQDSFVEVSPV
gi 8134698	PLDHRGYQSLSDSPPGPRVFTSEKRPLSIQDSFVEVSPV
890.....
MOL3a	-----CLGTEVA-----
MOL3b	-----CLGTEVA-----
gi 12248382	-----CLGTEVA-----
gi 7305469	-----ELGAEVA-----
gi 11641291	-----CLGTEVA-----
gi 12698035	CPRPRVRLGSEIRDSVV
gi 8134698	CPRPRVRLGSEIRDSVV

Table 3I lists the domain description from DOMAIN analysis results against MOL3. The region from amino acid residue 64 through 478 (SEQ ID NO:8) most probably (E = 1e⁻¹²¹) contains a PSI, domain found in Plexins, Semaphorins and Integrins, aligned here in Table

3I. Semaphorins are involved in growth cone guidance as well as other developmental processes. Plexins and integrins are involved in developmental processes. The MOL1 sequence likely has properties similar to those of other proteins known to contain this domain

Table 3I. Domain Analysis of MOL3

gnl|Smart|smart00423, PSI, domain found in Plexins, Semaphorins and Integrins
CD-Length = 431 residues, 100.0% aligned
Score = 430 bits (1106), Expect = 1e-121



The protein similarity information, expression pattern, cellular localization, and map location for the protein and nucleic acid for MOL3 suggest that this Semaphorin B-like protein may have important structural and/or physiological functions characteristic of the Semaphorin B family. This family is involved in developmental processes including growth cone guidance. MOL3 likely plays a similar role in those developmental processes. Therefore, the MOL3 nucleic acids and proteins are useful in potential diagnostic and therapeutic applications and as a research tool. These include serving as a specific or selective nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These also include potential therapeutic applications such as the following: (i) a protein therapeutic, (ii) a small molecule drug target, (iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a nucleic acid useful in gene therapy (gene delivery/gene ablation), (v) an agent promoting tissue regeneration *in vitro* and *in vivo*, and (vi) a biological defense weapon.

The MOL3 nucleic acids and proteins have applications in the diagnosis and/or treatment of various diseases and disorders. For example, the compositions of the present invention will have efficacy for the treatment of patients suffering from: neuronal developmental, organizational, mediated and interactive disorders and disease; endocrine dysfunctions, diabetes, obesity, growth and reproductive disorders, injury repair as well as other diseases, disorders and conditions.

These materials are further useful in the generation of antibodies that bind immuno-specifically to the novel MOL3 substances for use in therapeutic or diagnostic methods. These

antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-MOLX Antibodies" section below. The disclosed MOL3 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated MOL3 epitope is from about amino acids 30 to 100. In another embodiment, a MOL3 epitope is from about amino acids 110 to 150. In additional embodiments, MOL3 epitopes are from about amino acids 160 to 200, 210 to 230, 250 to 300, 350 to 400, 450 to 475, 500 to 575, 620 to 630, and from about amino acids 700 to 750. These novel proteins can also be used to develop assay systems for functional analysis.

10 MOL4

The disclosed novel semaphorin-like protein, MOL4 (also referred to herein as SC_111750277_A), is encoded by a nucleic acid, 6408 nucleotides long (SEQ ID NO:11). An open reading frame was identified beginning with an ATG initiation codon at nucleotides 1400-1402 and ending with a TGA codon at nucleotides 5456-5458. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table 4A, and the start and stop codons are in bold letters.

Table 4A. MOL4 Nucleotide Sequence (SEQ ID NO:11).

CCTGGGACTCTGGGAGAATGGTCCAGAGCTCATTGTCCTTGTGATAAAATGATAGATTGGACTCAATATCCCA
TGCTGCCTCTTCCAACCTGATTTTACCCAGACTGGGCTACCAGACTGGTATGCCACACATGCCGTTTCCTT
TCTTTCTTCTCTGCATCTCTGCCTTTGTGTCCAGAGCGTGTTCCTTTGCAAGTTTCTCTCCATTCTGCACA
TTATGAGTTTTCAGCATTTCTGTTGCCCTAGAAAGTCTATCTTTGAGATCTTGCACTGTTCTCTTTTACAGTGT
CTCATAAACTCCCTTCTTGGATTTCAGAACCACTTTCTTTCCCATTTATCCTGTCAAACCTGCTTCTTGCCATGGT
CCAGGGGTAGGAGGATGGCAGGCAGGAGGTGCTTCTCTGGGGCTCTTAGTGTCTCAATCTTCTGCTTTATCTGG
GTTTTCTTTTACCCAGAAATTTTATTATGTAAATGCTTCACTCAGACTTTGTTCTAATTATCCAATTTTGGCAT
ACTCTAGAAAGTCTTTGATATTTTCTTCTCCTCCAACCTATCTATTTTATTTTCATAGTTCTCTTTGGTTATCTC
TTAGAATCACACTTTCTGTTTAAATTTTCAAATCCTTTGTCTTTCTCACTCGTTCTTAGGTACCTTTTCTT
ACATTTTCAAATATATTTTGTTCAGCAGAGGGCTCCCTTCCATCCCTCTTGACGCCGGGCAGCTAGGATTT
GAACTTTGCCCTTGAATCTTTCTCTCCGCTTCTAGCCATCAGAAACACTAGATCACTTAAACTTGTAAACAA
TTCCGGCTCGCTCCTTGTGATTGCGCTAAACCTTCCGTCCTCAGCTGAGAACGCTCCACCACCTCCCGGATCGC
TCATCTCTTGGCTGCCCTCCCACTGTTCTGATGTTATTTTACTCCCGTATCCCTACTCGTTCTTCACAATTC
TGTAGGGTGGTATTACTAACCCAGTTTACAGCTGAGGAACTGAGGCTTGGAGAGGTTTGGTCCGTATCGTAC
AGTTTGCAAGGTTAACCTAATCCGGCCAGTTCTGGCTTTCCAGCCAGCCAGCAGCCTAGCCTCCCTCTCTGC
CGCTGCAGGTTATAACGGCTCTCCCCGTTTTACAGAGGTCCCTTCCCCTTCAAATCCACAGGCAGGAAGATCG
TTCCGAACCTGACGGGGCTGGGAATGTGGGAGTCCGAGTGGGGTTTGGGGGAGCTTCCCTCAGGCCCTGAGTGT
GGGGTGGGCAGGCCGCGCGATGGCCCTCGGGGATGTACATTCCAGATGGGGTGACCGAGAACGCAAGGCGGG
ATGTGGCAAACGGCGCAAGTCTCGGAGTCTTAGGTCTTGGCCGCGAATGCCGCGGGGAAGGGCTTCGGC
CCACCGGCTGGTCACCACTCGGCAGGCCCGGGCGGGAGTCCGCGGAGCAGCCGCGGATGCAGGGCGCCCC
CTCGCGCTCTCCGCGCGCTCGAGGCTGCGGGTGCAGCGCCGCGCGGAGGTCTGCTCCAGCCCCCTCTCTC
TTTTTGGTCCCGCTCCCTCTCTCTCCCTTTGCTTGCACACTCTCCCCACCGCCCCCTCTCTCTCTGCT
CCCGCGTCTCTCTCTCTCTCTCTCGAGCGCGGGTCCGGAGCTAGTTGGAGCGCGGGGGTGGTGCACAGA
GCCAGCTCCGCGAGCCGGGCGGGTCCGAGCGCATCCAGCGGCTGCTGGGAGCCGAGCGCAGCGGGCGCGGG
CCCGGGTGGGACTGCACCGAGCGCTGAGAGCTGGAGGCGGTTCTTGCAGCGCGCCCATTTCCAGACCGGCC
GCAGCCCATCTGGTTAGCTCCGCGCTCCGCGCGCGCGGAGTCCGGAGCCGCGGGGAACCGGCACCTGCA
CCCGCTCTGGGAGTGAGTGGTTCAGCTGGTGGCTGGCTGTGTCTTGGATGCCCTTGGCTTCACTCCGTC
TCCTGTTGCCACCACTCGTCCCTGGGCGGCTGATACCCAGCCCAACAGCTAAGGTGTGGATGGACAGTAGG
GGCTGGCTTCTCTCACTGGTCAAGGGTCTTCTCCCTGTCTGCCTCCCGAGCTAGGACTGCAGAGGGCCCTAT
CATGGTGTCTGAGGCCCCCTGGCTGTCTCGCTGTGTGCTGCCAGCCTCACACTGCTGGTGTCCACCTCTCCAG
CTCCAGGATGTCTCAGTGAGCCAGCAGTGAGCAGCAGCTGTGCGCCCTTAGCAAGCACCCACCGTGGCCTT
TGAAGACCTGCAGCCGTGGGTCTCTAACTTCACTACCTGGAGCCCGGATTTCTCCAGCTGGCTTTGGACCC

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CTCCGGGAACCAAGCTCATCGTGGGAGCCAGGAACCTACCTCTTCAGACTCAGCCTTGCCAATGTCTCTCTTCTTCA
GGCCACAGAGTGGGCTCCAGTGAGGACACGCGCGCTCTGCCAAAGCAAAGGGAAGACTGAGGAGGAGTGTCA
GAACTACGTGCGAGTCCGTATCGTCCGCGCGCGGAAGGTGTTTCATGTGTGGAACCAATGCCTTTTCCCCCATGTG
CACCAGCAGACAGGTGGGAACCTCAGCCGGACTACTGAGAAGATCAATGGTGTGGCCCGCTGCCCTATGACCC
ACGCCACAACCTCCACAGCTGTCTCTCCAGGGGAGCTCTATGCAGCCACGGTCATCGACTTCTCAGGTGCG
GGACCCTGCCATCTACCGCAGCCTGGGCGAGTGGGCCACCGCTTCGCACTGCCCAATATAACTCCAAGTGGCTTAA
TGAGCCAAACTTCGTGGCAGCCTATGATATTGGGCTGTTTGCATACTTCTTCTGCGGGAGAACGAGTGGAGCA
CGACTGTGGACGACACCGTGTACTCTCGCGTGGCCCGCTGTGCAAGAATGACGTGGGGGGCCGATTCTGTCTGGA
GGACACATGGACCAATTCATGAAGGCCCGCTCAACTGTCTCCGCGCGGGCGAGGTCCCTTCTACTATAACGA
GCTCAGAGTGCCTTCCACTTGCCAGAGCAGGACCTCATCTATGGAGTTTTCACAACCAACGTAACAGCATCGC
GGCTTCTGTCTGTGCGCCTTCAACCTCAGTGTCTATCTCCAGGCTTTCAATGGCCCAATTCGCTACCAGGAGAA
CCCCAGGGCTGCCTGGCTCCCCATAGCCAACCCCATCCCCAATTTCCAGTGTGGCACCTGCCTGAGACCGGTCC
CAACGAGAACCTGACGGAGCGCAGCTGCAGGACGCGCAGCGCTCTTCTGATGAGCGAGGCCGTGCAGCCGGT
GACACCCGAGCCTGTGTACCCAGGACAGCGTGCCTTCTCACACCTCGTGGTGGACCTGGTGCAGGCTAAAGA
CACGCTCTACCATGTACTCTACATTGGCACCGAGTCCGGCACCATCTGAAGGCGCTGTCCACGGCGAGCCGCGAG
CCTCCACGGCTGTACCTGGAGGAGCTGCACGTGCTGCCCGCGCGCGGAGCCCTGCGCAGCCTGCGCAT
CCTGCACAGCGCCCGCGCTCTTCTGTGGGCTGAGAGACGGCGCTCTGCGGGTCCCACTGGAGAGGTGCGCCG
CTACCGCAGCCAGGGGCGATGCTGGGGGCGGGGACCGTACTGTGGCTGGGACGGGAAGCAGCAACGTTGCAG
CACACTCGAGGACAGCTCCAACATGAGCCTCTGGACCCAGAACATCACCGCTGTCTGTGCGGAATGTGACAG
GGATGGGGGCTTGGGCCATGTCACCATGGCAACCATGTGAGCACTTGGATGGGGACAACCTCAGGCTCTTGCCT
GTGTGAGCTCGATCTGTGATTCCCTCGACCCGCTGTGTGGGGCTTGTGCTGCTGGGGCCAGCCATCCACAT
CGCCAATGTCTCAGGAATGGGGCGTGGACCCCGTGGTTCATCGTGGGCGCTGTGCAGCAGCTCCTGTGGCATCG
CTTCCAGGTCCGCCAGCGAAGTTGCAGCAACCTGTCTCCCGCCACGGGGCGCGCATCTGCGTGGGCAAGAGCCG
GGAGGAACCGTTCTGTAATGAGAAACAGCCTTGCCCGGTGCCCATCTTCTGGGCTTCTTGGGGCTCCTGGAGCAA
GTGCAGCAGCAACTGTGGAGGGGGCATGCACTGCGCGCTCGGGCTGCGAGAACGGCAACTCCTGCTGGGCTG
CGGCGTGGAGTTCAAGACGTGCAACCCCGAGGGCTGCCCGAAGTGGCGCGCAACACCCCTGGACGCGGTGGCT
GCCCGTGAACGTGACGCGAGGGCGGGGACGCGCAGGAGCAGCGGTTCCGCTTCACTGCGCGCGCCCTTGCAGA
CCCGCAGCGCTGCAGTTCGGCAGGAGAAGGACCGAGACGAGGACCTGTCCCGCGGACGGCTCCGGCTCCTGCGA
CACCGACGCCCTGGTGGAGGACCTCTGCGCAGCGGGAGCACCTCCCGCACACGGTGAGCGGGGGCTGGGCCG
CTGGGGCCCGTGGTCTGTCTCTGCTCCCGGAGTGCAGCTGGGGCTTCCGCGTCCGCAAGAGAACGTGCACTAACCC
GGAGCCCCGCAACGGGGGCTGCCCTGCGTGGGCGATGCTGCCGAGTACCAGGACTGCAACCCCGAGGCTTGCCC
AGTTGCGGGTCTTGGTCTGTGACCTCATGGTCTCATGTCTAGCTTCTGTGGTGGGGCTCACTACTCAACG
CACCGTTCCTGCACACGCCCCGACCCCTCCCGAGGTGAGGACATCTGTCTCGGGCTGCACACGGAGGAGGCACT
ATGTGCCACACAGCCCTGCCAGAGGGCTGGTGCCTGTGTGAGTGGAGTAAGTGCACTGACGACGGAGCCCA
GAGCCGAAGCCGGCACTGTGAGGAGCTCCTCCAGGGTCCAGCGCTGTGTGGAACAGCAGCCAGAGCCGCCC
CTGCCCTACAGCGAGATTCCCGTCTCTGCCAGCCTCCAGCATGGAGGAGGCCACCGCTGTGCAGGGTTCAA
TCTCATCCACTGGTGGCCACGGGCATCTCTGCTTCTTGGGCTTGGGCTCTGACCCCTAGCAGTGTACTGTG
TTGCCAGCACTGCCAGCGTCAGTCCAGGAGTCCACACTGGTCCATCTGCCACCCCAACCACTTGCACACTACA
GGCGGAGGACCCCCGAAGAATGAAAAGTACACACCCATGGAATTCAAGACCCTGAACAAGAATAACTTGATCCC
TGATGACAGAGCCAACCTTCTACCCATTGCAGCAGACCAATGTGTACAGACTACTTACTACCCAAGCCCCCTGAA
CAAACACAGCTTCCGGCCCGAGGCCTCACCTGGACAACGGTGTCTCCCAACAGCTGATACCGCGCTCCTGGGA
CTTGGGCTTCTTGCCTTATAAGGCACAGAGCAGATGGAGTGGGACAGTGGAGCCAGTTTGGTTTCTCCCTCT
GCCTAGGCCAAGAACCTTGTCTGCTTGCCTTGGGGGCTCCCATCCGGCTTCAGAGAGCTCTGGCTGGCATTGAC
CATGGGGGAAAGGGCTGGTTTTCAGGCTGACATATGGCCGAGGTCCAGTTTCAGCCAGGTCTCTCATGGTTATCT
TCCAACCCACTGTACGCTGACACTATGCTGCCATGCTGGGCTGTGGACCTACTGGGCATTTGAGGAACGGAG
AATGGAGATGGCAAGAGGGCAGGCTTTTAAGTTTGGGTGGAGACAACTTCTGTGGCCCCCAAGCTGAGTCT
GGCCTTCTCCAGCTGGCCCAAAAAGGCTTTGCTACATCTGTATTATCTTGAAAGTAATCAATCAAGTGGCT
CCAGTAGCTCTGGATTTCTGCCAGGGCTGGGCCATTGTGGTGTGCCCCAGTATGACATGGGACCAAGGCCAGC
GCAGGTATCCACCTCTGCCTGGAAGTCTATACTCTACCCAGGGCATCCCTCTGGTTCAGAGGCACTGAGTACTGG
GAACCTGGAGGCTGACCTGTGCTTAGAAGTCTTTAATCTGGGCTGGTACAGGCCTCAGCCTTGCCCTCAATGCAC
GAAAGGTGGCCAGGAGAGAGGATCAATGCCACAGGAGGCAGAAGTCTGGCTCTGTGCTCTATGGAGACTATC
TTCCAGTTGTGCTCAACAGAGTTGTTGGCTGAGACCTGCTTGGGAGTCTGTGCTGGCCCTTCTCTGTTTCAGGA
ACACACACACACACACTCAACACGACACACAATCACAATTGCTACAGCAACAAAAAAGACATTGGGCTGT
GGCATTATTAATTAAGATGATATCCAGTCTCC

```

The 1352 amino acid MOL4 polypeptide (SEQ ID NO:12) encoded by SEQ ID NO:11 is presented using the one-letter amino acid code in Table 4B. The Psort profile for MOL4 predicts that this sequence has no signal peptide and is likely to be localized in the plasma membrane with a certainty of 0.7900. MOL4 has a molecular weight of 145674.1 Daltons.

Table 4B. MOL4 protein sequence (SEQ ID NO:12)

```

MPAGEGASAHRAHHTRQARGGSRPSSRGMQGAPSRSSARLEAGGCSARRGRSAPAPSSFSLLPLPSFSPFACNSSP
TAPSLILLPRSPPPCSLRAPGRRLVGARGLVPEPSSAEPGGSAAHAAAGSPSAAGAGPGDCTGALRAGGRSCAA
APFPDRPPAHLVSSRRSAPPSPGSRPRGTGHLHPPLGVSGSSWCLACVSWMPCGFSPPVAHHLVPGPPDTPAQQLR
CGWTVGGWLLSLVRGLLPCLPPGARTAEGLIMVLGAPLAVSLLLPSLTLVSHLSSSQDVSEPSSEQQLCALSKH
PTVAFEDLQPVWSNFTYPGARDPSQLALDPSGNQLIVGARNYLFRLSLANVSLQATEWASSEDTRRSQSKGKTE
BECQNYVRVLIVAGRKVFMCCTNAFSPMCTSRQVGNLSRTTEKINGVARCPYDPRHNSTAVISSQGEIYAATVIDF
SGRDPPIYRSLGSGPPLRTAQYNSKWLNEPNFVAAYDIGLFAYFFLRENAVEHDCGRTVYSRVARVCKNDVGGRL
LEDTWTTTFMKARLNCSPGEPVFFYNEQLQSAFHLPEQDLIYGVFTTNVNSIAASAVCAFNLSAISQAFNGPFRYQE
NPRAAWLPPIANPIPNFQCGTLPETGPNENLTERSLQDAQRLFLMSRAVQPVTPPCVTVQDSVRFSLVVDLVQAKD
TLYHVLVYIGTESGTILKALSTASRSLHGCYLEELHVLPPGRREPLRLRILHSARALFVGLRDGVLRVPLERCAAY
RSQGACLGARDPYCGWDGKQQRCTLEDSSNMSLWTONITACPVNRVTRDGGFGPWSWPQCEHLGDNSGSCLCR
ARSCDSPRPRCGGLDCLGPAIHIANCSRNGAWTPWSSWALCSTSCGIFQVRQRSCSNPAPRHGGRICVGKSRER
FCNENTPCVPPIFWASWGSWSKCSNCGGMQSRRRACENGNSCLGCGVEFKTCNPEGCPVEVRNTPFWTPWLPVNV
TQGGARQEQRFRTCTRAPLADPHGLQFGRRTTETRTCPADGSGSCDLDALVEDLLRSGSTSPHTVSGGWAANGPWS
SCSRDCELGFRVRKRTCTNPEPRNGGLPCVGDAEYQDCNPQACPVRGAWSCWTSWSPCSASCAGGGHYQTRTSCTS
PAPSPGEDICLGLHTEALCATQACPEGWSPWSEWSKCTDDGAQSRSRHCEELLPGSSACAGNSSQSRPCPYSEIP
VILPASSMEEATGCAGFNLIHLVATGISCFGLGSLTLAVYLSQHCQRQSQESTLVHPATPNHLHYKGGGTPKNE
KYTPMEFKTLNKNLI PDDRANFYPLQQINVTYTTTYPSPLNKHSFRPEASPGQRCFPNS

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The disclosed nucleic acid MOL4 sequence has 3226 of 3664 bases (88%) identical to a *Mus musculus* semaphorin mRNA (GENBANK-ID: ACC: X97818).

The full amino acid sequence of the disclosed MOL4 polypeptide has 1021 of 1093 amino acid residues (93%) identical to, and 1053 of 1093 residues (96%) positive with, the 1093 amino acid residue semaphorin 5B precursor protein from *Mus musculus* (ptnr:SPTREMBL-ACC:Q60519), and 971 of 973 amino acid residues (99%) identical to, and 972 of 973 residues (99%) positive with patp:AA94990 Human secreted protein vb21_1, having 999 aa. The C-terminal 1202 amino acid residues of MOL4 are 100% identical to human KIAA1445 PROTEIN (TREMBLNEW-ACC:BAA95969).

MOL4 expression in different tissues was examined through TaqMan as described below in Example 1.

A SNP for MOL4 and the corresponding amino acid change it would cause is shown in Table 4C. The SNP was identified using the techniques disclosed in Example 3.

Table 4C: SNP for MOL4			
Consensus Position	Base Change	AA Change Position	Residue Change
2046	C > T	682	A > V

In a search of CuraGen's proprietary human expressed sequence assembly database, assemblies 111750277 (589 nucleotides) and 87739769 (896 nucleotides) were identified as having >95% homology to this predicted semaphorin sequence (Fig 3A2). This database is composed of the expressed sequences (as derived from isolated mRNA) from more than 96 different tissues. The mRNA is converted to cDNA and then sequenced. These expressed

DNA sequences are then pooled in a database and those exhibiting a defined level of homology are combined into a single assembly with a common consensus sequence. The consensus sequence is representative of all member components. Since the nucleic acid of the described invention has >95% sequence identity with the CuraGen assembly, the nucleic acid of the invention likely represents an expressed semaphorin sequence.

The DNA assembly 111750277 has 3 components and was found by CuraGen to be expressed in the following tissues: Lymph node and Lung. The DNA assembly 87739769 has 7 components and was found by CuraGen to be expressed in the following tissues: Brain, Uterus, and Lung.

BLASTP (Non-Redundant Composite database) analysis of the best hits for alignments with MOL4 are listed in Table 4D.

Table 4D. BLASTP results for MOL4					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 7305473 ref NP_038689.1	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem [Mus musculus])	1093	1021/1093 (93%)	1053/1093 (95%)	0.0
gi 7959149 dbj BAA95969.1 (AB040878)	KIAA1445 protein [Homo sapiens]	1202	1202/1202 (100%)	1202/1202 (100%)	0.0
gi 4506881 ref NP_003957.1	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A; semaphorin F; sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM)	1074	616/1043 (59%)	781/1043 (74%)	0.0
gi 12731706 ref XP_004042.2	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A [Homo sapiens]	1074	617/1043 (59%)	781/1043 (74%)	0.0
gi 6677915 ref NP_033180.1	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem; M-Sema D [Mus musculus])	1077	617/1046 (58%)	776/1046 (73%)	0.0

This information is presented graphically in the multiple sequence alignment given in Table 4E (with MOL4 being shown on line 1) as a ClustalW analysis comparing MOL4 with related sequences.

Table 4E Information for the ClustalW proteins:

1) MOL4 (SEQ ID NO:12)
2) gi|12731706|ref|XP_004042.2| sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A [Homo sapiens] (SEQ ID NO:41)
3) gi|7305473|ref|NP_038689.1| sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem [Mus musculus] (SEQ ID NO:42)
4) gi|6677915|ref|NP_033180.1| sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem; M-Sema D [Mus musculus] (SEQ ID NO:43)
5) gi|4506881|ref|NP_003957.1| sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A; semaphorin F; sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) (SEQ ID NO:44)
6) gi|7959149|dbj|BAA95969.1| (AB040878) KIAA1445 protein [Homo sapiens] (SEQ ID NO:45)

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65

MOL4
gi|12731706|
gi|7305473|
gi|6677915|
gi|4506881|
gi|7959149|

10 20 30 40 50
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
MPAGEGASAHRRAGHHTROARGGSRPSSRGMOGAPSRSSARLEAGGCSARR
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|

MOL4
gi|12731706|
gi|7305473|
gi|6677915|
gi|4506881|
gi|7959149|

60 70 80 90 100
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
GRSAPAPSSFSLLPLPSFPFACNSSPTAPSLLLLPRSPPPCSLRAPGREL
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
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MOL4
gi|12731706|
gi|7305473|
gi|6677915|
gi|4506881|
gi|7959149|

110 120 130 140 150
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
VGARGLVPEPSSAEPGSSAAHPAAAGSPSAAGAGPGDCTGALRAGGRSC
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
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MOL4
gi|12731706|
gi|7305473|
gi|6677915|
gi|4506881|
gi|7959149|

160 170 180 190 200
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
AAAPFPDRPPAHLVSSRRSAPPGPSREPRGTGHLHPPLGVSGSSWCLACVS
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
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MOL4
gi|12731706|
gi|7305473|
gi|6677915|
gi|4506881|
gi|7959149|

210 220 230 240 250
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
WMPCGFSPSPVAHHLVPGPPDTPAQQLRCGWTVGGWLLSLVRGLLPCLFP
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|

MOL4
gi|12731706|
gi|7305473|

	gi 6677915	-----
	gi 4506881	-----
	gi 7959149	WMPCGFSPSPVAHHLVPGPPDTFAQQRLRCGWIVGGWLLSLVRGLLPCLPP
5		260 270 280 290 300
	MOL4	GARTAEGPIMVIAAGPLAVSLLLPSLTLLVSHLSSSDVSSEPSSEQQLCA
	gi 12731706	-----MKGTCVIAWLFSSLGWR-----LAHPEAQCTTCCQ
10	gi 7305473	-----MVPFGPLATSLTSSLTLLVSHLSSSDIASESSSEQQMCT
	gi 6677915	-----MKGACILAWLFSSLGWR-----LARPETONPAKCO
	gi 4506881	-----MKGTCVIAWLFSSLGWR-----LAHPEAQCTTCCQ
	gi 7959149	GARTAEGPIMVIAAGPLAVSLLLPSLTLLVSHLSSSDVSSEPSSEQQLCA
15		310 320 330 340 350
	MOL4	LSKHETVAFEDLOPVVSNFTYPCARDFSQALDPSGNOLLVGCARNYLFRL
	gi 12731706	-----RTEHPVLSYKELCPMLREBRAKNAVDPSQLTFDPCQKELVGCARNYLFRL
	gi 7305473	-----RREHPTVAFEDLKPVVFNFTYPGVRDFSQALDPSGNOLLVGCARNYLFRL
20	gi 6677915	-----RAEHFVVSYKELCPMLREBRAKNAVDPSQLTFDPCQKELVGCARNYLFRL
	gi 4506881	-----RTEHPVLSYKELCPMLREBRAKNAVDPSQLTFDPCQKELVGCARNYLFRL
	gi 7959149	LSKHETVAFEDLOPVVSNFTYPCARDFSQALDPSGNOLLVGCARNYLFRL
25		360 370 380 390 400
	MOL4	SLANVSLQAWEWASSEDTRRSQCSKGTTEBECQNYVRVLIVAGRKVEMC
	gi 12731706	-----QLEDLSLQAWEWECDEATKKACYSKGSKEBECQNYVRVLIVAGRKVEMC
	gi 7305473	-----SLANVSLQAWEWASSEDTRRSQCSKGTTEBECQNYVRVLIVAGRKVEMC
30	gi 6677915	-----ELEDLSLQAWEWECDEATKKACYSKGSKEBECQNYVRVLIVAGRKVEMC
	gi 4506881	-----QLEDLSLQAWEWECDEATKKACYSKGSKEBECQNYVRVLIVAGRKVEMC
	gi 7959149	SLANVSLQAWEWASSEDTRRSQCSKGTTEBECQNYVRVLIVAGRKVEMC
35		410 420 430 440 450
	MOL4	GTNAFSPVCTISROVGNLSRTIEKINGVARCYPDPRHNSTAVISSQCELYA
	gi 12731706	-----GTNAFTPVCTINRSISNLBRIHDQISGMARCPYSPCHNSTALLTAGGELYA
	gi 7305473	-----GTNAFSPVCSROVGNLSRTIEKINGVARCYPDPRHNSTAVISSQCELYA
	gi 6677915	-----GTNAFTPVCTISROVGNLSRTIEKINGVARCYPDPRHNSTALLTAGGELYA
	gi 4506881	-----GTNAFTPVCTINRSISNLBRIHDQISGMARCPYSPCHNSTALLTAGGELYA
40		460 470 480 490 500
	MOL4	ATVDFSGRDPATYRSLGCPPLRTAQYNSKWLNEPNFVAAYDIGLEAFYF
	gi 12731706	-----ATAMDFEGRDPATYRSLGILPPLRTAQYNSKWLNEPNFVSSYDIGNFTYF
45	gi 7305473	-----ATVDFSGRDPATYRSLGCPPLRTAQYNSKWLNEPNFVAAYDIGLEAFYF
	gi 6677915	-----ATAMDFEGRDPATYRSLGILPPLRTAQYNSKWLNEPNFVSSYDIGNFTYF
	gi 4506881	-----ATAMDFEGRDPATYRSLGILPPLRTAQYNSKWLNEPNFVSSYDIGNFTYF
	gi 7959149	ATVDFSGRDPATYRSLGCPPLRTAQYNSKWLNEPNFVAAYDIGLEAFYF
50		510 520 530 540 550
	MOL4	FLRENAVEHDCGRTVMRSVARVCKNDIGGRFLEDWTTFMKARLNCSR
	gi 12731706	-----FLRENAVEHDCGKTVMRSVARVCKNDIGGRFLEDWTTFMKARLNCSR
55	gi 7305473	-----FLRENAVEHDCGRTVMRSVARVCKNDIGGRFLEDWTTFMKARLNCSR
	gi 6677915	-----FLRENAVEHDCGKTVMRSVARVCKNDIGGRFLEDWTTFMKARLNCSR
	gi 4506881	-----FLRENAVEHDCGKTVMRSVARVCKNDIGGRFLEDWTTFMKARLNCSR
	gi 7959149	FLRENAVEHDCGRTVMRSVARVCKNDIGGRFLEDWTTFMKARLNCSR
60		560 570 580 590 600
	MOL4	GEVFFYYNELQSAPHLPECDLIYGVFTTNVNSIAASAVCAFNLSAISQAF
	gi 12731706	-----GEVFFYYNELQSTFELPELDLIYGVFTTNVNSIAASAVCFNLSAIAQAF
	gi 7305473	-----GEVFFYYNELQSAPHLPECDLIYGVFTTNVNSIAASAVCAFNLSAISQAF
65	gi 6677915	-----GEVFFYYNELQSTFELPELDLIYGVFTTNVNSIAASAVCFNLSAISQAF
	gi 4506881	-----GEVFFYYNELQSTFELPELDLIYGVFTTNVNSIAASAVCFNLSAIAQAF
	gi 7959149	GEVFFYYNELQSAPHLPECDLIYGVFTTNVNSIAASAVCAFNLSAISQAF
70		610 620 630 640 650
	MOL4	NGPFRYQENPRAAWLEIANPIPNFQCGLTPETGPNENLTERSLQDACLRF
	gi 12731706	-----SGPFRYQENSRSAWLPYPNPDPFQCGLTV-DQGLYVNLTERNLQDACLFI
	gi 7305473	-----NGPFRYQENPRAAWLEIANPIPNFQCGLTPETGPNENLTERSLQDACLRF
	gi 6677915	-----NGPFRYQENSRSAWLPYPNPDPFQCGLTV-DQGLYVNLTERNLQDACLFI
	gi 4506881	-----SGPFRYQENSRSAWLPYPNPDPFQCGLTV-DQGLYVNLTERNLQDACLFI
75		660 670 680 690 700
	gi 7959149	NGPFRYQENPRAAWLEIANPIPNFQCGLTPETGPNENLTERSLQDACLRF

5	MOL4	LMSEAVQPVTPPECVTQDSVRFSLVVDLVCAKDTLVEVLYIGTHSGTIL
	gi 12731706	LMHEVVQPVTTTFSFMDNSRFSLVAVDWWCGREALVHITMADTYGTIK
	gi 7305473	LMSEAVQPVTPPECVTQDSVRFSLVVDLVCAKDTLVEVLYIGTHSGTIL
	gi 6677915	LMHEVVQPVTTTFSFMDNSRFSLVAVDWWCGREALVHITMADTYGTIK
	gi 4506881	LMHEVVQPVTTTFSFMDNSRFSLVAVDWWCGREALVHITMADTYGTIK
10	MOL4 710 720 730 740 750
	gi 12731706	KALSTASRLHGCYLEELHVLPGRRERLRLSLILHSARALFVGLDGM
	gi 7305473	KVRVPLNQTSSSCLLEELHVLPGRRERLRLSLILHSARALFVGLDGM
	gi 6677915	KALSTASRLHGCYLEELHVLPGRRERLRLSLILHSARALFVGLDGM
	gi 4506881	KVRVPLNQTSSSCLLEELHVLPGRRERLRLSLILHSARALFVGLDGM
15	MOL4 760 770 780 790 800
	gi 12731706	KVPLKRCQFVTRSTCIGACDPYCGWDVVMKKCTSLLESLSTQDCESTIS
	gi 7305473	KVPLKRCQFVTRSTCIGACDPYCGWDVVMKKCTSLLESLSTQDCESTIS
	gi 6677915	KVPLKRCQFVTRSTCIGACDPYCGWDVVMKKCTSLLESLSTQDCESTIS
	gi 4506881	KVPLKRCQFVTRSTCIGACDPYCGWDVVMKKCTSLLESLSTQDCESTIS
20	MOL4 810 820 830 840 850
	gi 12731706	ACEVRNVIRCGGFGKSEWQCEHLDDGNSGSCLCRAKSCDSRPFCGGIL
	gi 7305473	ACEVRNVIRCGGFGKSEWQCEHLDDGNSGSCLCRAKSCDSRPFCGGIL
	gi 6677915	ACEVRNVIRCGGFGKSEWQCEHLDDGNSGSCLCRAKSCDSRPFCGGIL
	gi 4506881	ACEVRNVIRCGGFGKSEWQCEHLDDGNSGSCLCRAKSCDSRPFCGGIL
25	MOL4 860 870 880 890 900
	gi 12731706	DCLGPAHIANCSRNGATFWSWPCSTSCGIGFCVRQSCSNFAPPHG
	gi 7305473	DCLGPAHIANCSRNGATFWSWPCSTSCGIGFCVRQSCSNFAPPHG
	gi 6677915	DCLGPAHIANCSRNGATFWSWPCSTSCGIGFCVRQSCSNFAPPHG
	gi 4506881	DCLGPAHIANCSRNGATFWSWPCSTSCGIGFCVRQSCSNFAPPHG
30	MOL4 910 920 930 940 950
	gi 12731706	GRICVCKRREERFCKENTPCFVRLTFASAGSWKSSNCGGGVCSRRFAC
	gi 7305473	GRICVCKRREERFCKENTPCFVRLTFASAGSWKSSNCGGGVCSRRFAC
	gi 6677915	GRICVCKRREERFCKENTPCFVRLTFASAGSWKSSNCGGGVCSRRFAC
	gi 4506881	GRICVCKRREERFCKENTPCFVRLTFASAGSWKSSNCGGGVCSRRFAC
35	MOL4 960 970 980 990 1000
	gi 12731706	ENGNSCLCCGVEEKTCNPECCPEVRRNTFWTFWLPVNVTOGGARQEQRF
	gi 7305473	ENGNSCLCCGVEEKTCNPECCPEVRRNTFWTFWLPVNVTOGGARQEQRF
	gi 6677915	ENGNSCLCCGVEEKTCNPECCPEVRRNTFWTFWLPVNVTOGGARQEQRF
	gi 4506881	ENGNSCLCCGVEEKTCNPECCPEVRRNTFWTFWLPVNVTOGGARQEQRF
40	MOL4 1010 1020 1030 1040 1050
	gi 12731706	HTCRPLADPHGLQFGRRTETETCPADGSGSCDTALVEDLLSGSTSP
	gi 7305473	HTCRPLADPHGLQFGRRTETETCPADGSGSCDTALVEDLLSGSTSP
	gi 6677915	HTCRPLADPHGLQFGRRTETETCPADGSGSCDTALVEDLLSGSTSP
	gi 4506881	HTCRPLADPHGLQFGRRTETETCPADGSGSCDTALVEDLLSGSTSP
45	MOL4 1060 1070 1080 1090 1100
	gi 12731706	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 7305473	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 6677915	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 4506881	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
50	MOL4
	gi 12731706	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 7305473	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 6677915	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 4506881	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
55	MOL4
	gi 12731706	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 7305473	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 6677915	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 4506881	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
60	MOL4
	gi 12731706	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 7305473	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 6677915	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 4506881	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
65	MOL4
	gi 12731706	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 7305473	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 6677915	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 4506881	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
70	MOL4
	gi 12731706	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 7305473	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 6677915	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 4506881	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
75	MOL4
	gi 12731706	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 7305473	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 6677915	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY
	gi 4506881	HTVNGAASAWTSQCSRDGSRGIDNRKRVCNPPERRNGCLPCVGDAAEY

Tables 4F-4K list the domain descriptions from DOMAIN analysis results against MOL4. The region from amino acid residue 327 through 725 (SEQ ID NO:12) most probably ($E = 2e^{-118}$) contains a Sema domain found in Semaphorins, aligned here in Table 4F.

60 Semaphorins are involved in growth cone guidance, axonal pathfinding, and other developmental processes. The region from amino acid residue 1057 through 1109 (SEQ ID NO:12) most probably ($E = 3e^{-9}$) contains a Thrombospondin type-1 repeat found in thrombospondin-1 that binds to and activates TGF-beta, aligned here in Table 4G. TGF-beta is involved in the modulation of proliferation in many cell types. The region from amino acid

65 residue 868 through 921 (SEQ ID NO:12) most probably ($E = 4e^{-8}$) also contains a

Thrombospondin type-1 repeat found in thrombospondin-1 that binds to and activates TGF-beta, aligned here in Table 4H. The region from amino acid residue 926 through 972 (SEQ ID NO:12) most probably ($E = 6e^{-7}$) also contains a Thrombospondin type-1 repeat found in thrombospondin-1 that binds to and activates TGF-beta, aligned here in Table 4I. The region from amino acid residue 1169 through 1210 (SEQ ID NO:12) most probably ($E = 0.001$) also contains a Thrombospondin type-1 repeat found in thrombospondin-1 that binds to and activates TGF-beta, aligned here in Table 4J. The region from amino acid residue 756 through 803 (SEQ ID NO:12) most probably ($E = 1e^{-5}$) also contains a Thrombospondin type-1 repeat found in thrombospondin-1 that binds to and activates TGF-beta, aligned here in Table 4K. The presence of these domains indicates that the MOL4 sequence has properties similar to those of other proteins known to contain these domains.

Table 4F. Domain Analysis of MOL4

gnl|Smart|smart00630, Sema, semaphorin domain
CD-Length = 430 residues, 99.8% aligned
Score = 420 bits (1080), Expect = 2e-118

[illegible]

MOL4_1
Smart|smart00630 GCYLEEEHHVLPF--RRREERSTRILHSA
SVVLEETISVFPF--G--SPISDLIVESEPKK (SEQ ID NO:91)

Table 4G. Domain Analysis of MOL4

gnl|Smart|smart00209, TSP1, Thrombospondin type 1 repeats; Type 1 repeats in thrombospondin-1 bind and activate TGF-beta.
CD-Length = 51 residues, 100.0% aligned
Score = 58.2 bits (139), Expect = 3e-09

MOL4_3
Smart|smart00209
10 20 30 40 50
AAAGPWSSCSRDCELG--FRVEKRP--TCTNPEPR--GGLPCVGDAAEYQD
WGEWSEWSPCSVTCCG--VQTRIP--CONP--EPN--GGGFCITCPDTETRA

MOL4_3
Smart|smart00209
15
CNPO-ACP
CNPO-PCP (SEQ ID NO:92)

Table 4H. Domain Analysis of MOL4

gnl|Smart|smart00209, TSP1, Thrombospondin type 1 repeats; Type 1 repeats in thrombospondin-1 bind and activate TGF-beta.
CD-Length = 51 residues, 100.0% aligned
Score = 54.3 bits (129), Expect = 4e-08

MOL4_4
Smart|smart00209
20 30 40 50
RTFWSSEALCSTSCGIGGVVQVPSCEINAPRHGGRICVCKSRSEFFCNFN
WGEWSEWSPCSVTCCG--VQTRIP--CONP--EPN--GGGFCITCPDTETRA

MOL4_4
Smart|smart00209
25
TCPC
-PCP (SEQ ID NO:93)

Table 4I. Domain Analysis of MOL4

gnl|Smart|smart00209, TSP1, Thrombospondin type 1 repeats; Type 1 repeats in thrombospondin-1 bind and activate TGF-beta.
CD-Length = 51 residues, 100.0% aligned
Score = 50.4 bits (119), Expect = 6e-07

MOL4_5
Smart|smart00209
30 40 50
RSCWISWSPCSASCSCGG--HYQRTN--SCTSPAES--PCRDICLGLH
WGEWSEWSPCSVTCCG--VQTRIP--CC--NPEP--NGGGFCITCPD

MOL4_5
Smart|smart00209
35
TEEALCATC-ACP
TEETRAQNEC-PCP (SEQ ID NO:94)

Table 4J. Domain Analysis of MOL4

gnl|Smart|smart00209, TSP1, Thrombospondin type 1 repeats; Type 1 repeats in thrombospondin-1 bind and activate TGF-beta.
CD-Length = 51 residues, 88.2% aligned
Score = 39.7 bits (91), Expect = 0.001

MOL4_6
Smart|smart00209
40 50
WASWGSNSKCSNCGGG--MCSRRR--AC--E--NENSCLCGVVEFKCN
WGEWSEWSPCSVTCCG--VQTRIP--CONPPN--GGGFCITCPDTETRA

MOL4_6
Smart|smart00209 EQ-PCF (SEQ ID NO:95)

Table 4K. Domain Analysis of MOL4

gnl|Pfam|pfam01437, Plexin_repeat, Plexin repeat
CD-Length = 48 residues, 100.0% aligned
Score = 46.2 bits (108), Expect = 1e-05

MOL4_8
Pfam|pfam01437

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.....|
RCAAY-RSQACICARF-FVCGFDGKGCRCATLEDSNNMS-----LHHC
NCSQH-TSCSSCLSAPE-FGCCWCPSHKRCARLEHCSRGE-----GMSQ

MOL4_8
Pfam|pfam01437

10

15

20

25

30

35

40

45

50

.....|
NITACE
SSETCE (SEQ ID NO:96)

The above defined information for MOL4 suggests that this semaphorin-like protein may function as a member of a "Semaphorin family". Therefore, the novel nucleic acids and proteins identified here may be useful in potential therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated below. The potential therapeutic applications for MOL4 include, but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, tissue regeneration *in vivo* and *in vitro* of all tissues and cell types composing (but not limited to) those defined here.

The MOL4 nucleic acids and proteins are useful in potential therapeutic applications implicated in Parkinson's disease, psychotic and neurological disorders, Alzheimers disease, cancer including but not limited to lung or breast cancer, endocrine disorders, inflammatory disorders, gastro-intestinal disorders and disorders of the respiratory system, and/or other pathologies and disorders. For example, a cDNA encoding the semaphorin-like protein may be useful in gene therapy, and the semaphorin-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from Parkinson's disease, psychotic and neurological disorders, Alzheimers disease, cancer including but not limited to lung or breast cancer, endocrine disorders, inflammatory disorders, gastro-intestinal disorders and disorders of the respiratory system. MOL4, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

These materials are further useful in the generation of antibodies that bind immuno-specifically to the novel MOL4 substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from

hydrophobicity charts, as described in the "Anti-MOLX Antibodies" section below. The disclosed MOL4 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated MOL4 epitope is from about amino acids 5 to 75. In another embodiment, a MOL4 epitope is from about amino acids 100 to 200. In additional embodiments, MOL4 epitopes are from about amino acids 300 to 375, 420 to 600, 600 to 675, 775 to 850, 900 to 1150, , and from about amino acids 1250 to 1350. These novel proteins can also be used to develop assay systems for functional analysis.

MOL5

10 MOL5a

The disclosed novel semaphorin 4C -like nucleic acid of 3868 nucleotides, MOL5a, (also referred to as SC20422974-A) is shown in Table 5A. An ORF begins with an ATG initiation codon at nucleotides 453-455 and ends with a TGA codon at nucleotides 2952-2954. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 5A, and the start and stop codons are in bold letters.

Table 5A. MOL5a Nucleotide Sequence (SEQ ID NO:13)

CGACTATCCATGAAGCCCGAGCCCCAGTGGCTGCAAGGCCTGCTGCCTGAGGTTCTTTCAAGAACTCAAACCT
CTTAGGCCTGAGTGTGTATGTTGGGCGGGGGTCCCCTTTTATTTCTCAAATGATTTCTGTGCGCAGAGGTAG
TGGTGGGTCTGAGGCCAGGGAGGGCTTCCCGAGCCTGTTAGCCTTCAGCCAACTCAACTCCTCCCCGCTTCC
CAGGGAGACCTGTGGTCTTTAGGCAGAGGCCAAGTGTGGGACTTAGGTCCACCTCCAAAGAGAAGGGGAAGGA
GGGCACCGGGCTCCTGGAAGGCCTGATGAGGAGTCTGTGGCCTCTCCTGCTGCGGGCCCCCTCTGTTTGTCTT
CTCTGGCTGTGATTTCTGACCATGTCTTTCCCTCAGCAGGACAGCTGGCCTGAAGCTCAGAGCCGGGGCTGCG
CCATGGCCCCACACTGGGCTGTCTGGCTGCTGGCAGCAAGGCTGTGGGGCCTGGGCATTGGGGCTGAGGTGTGGT
GGAACCTTGTGCCGCGTAAGACAGTGTCTTCTGGGGAGCTGGCCACGGTAGTACGGCGGTTCTCCAGACCGGCA
TCCAGGACTTCTGACACTGACGCTGACGGAGCCCACTGGGCTTCTGTACGTGGGCGCCGAGAGGCGCTGTTTG
CCTTCAGTGTAGAGGCTCTGGAGCTGCAAGGAGCGATCTCCTGGGAGGCCCGCTGGAGAAGAAGACTGAGTGT
TCCAGAAAGGGAAGAACAACAGACCGAGTGCTTCAACTTCATCCGCTTCTGACGCCCTACAATGCCTCCCACC
TGTACGTCTGTGGCACCTACGCCTTCCAGCCCCAAGTGCACCTACGTCAACATGCTCACCTTCACTTTGGAGCATG
GAGAGTTTGAAGATGGGAAGGGCAAGTGTCCCTATGACCCAGCTAAGGGCCATGCTGGCCTTCTTGTGGATGGTG
AGCTGTACTCGGCCACACTCAACAACTTCTGGGCACGGAACCCATTATCCTGCGTAACATGGGGCCCCACCACT
CCATGAAGACAGAGTACCTGGCCTTTGGCTCAACGAACCTCACTTGTAGGCTCTGCCCTATGTACCTGAGAGTG
TGGGCAGCTTCACGGGGACGACGACAAGGTCTACTTCTCTTCAGGGAGCGGGCAGTGGAGTCCGCCTGCTATG
CCGAGCAGGTGTGGCTCGTGTGGCCCGTGTCTGCAAGGCGATATGGGGGGCGCACGGACCCTGCAGAGGAAGT
GGACCACGTTCTGAAGGCGCGGTGGCATGCTGCCCCGAACCTGGCAGCTCTACTTCAACCAGCTGCAGGCGA
TGCACACCCTGCAGGACACCTCCTGGCACAACACCACCTTCTTTGGGGTTTTTCAAGCACAGTGGGTGACATGT
ACCTGTGCGCCATCTGTGAGTACCAAGTTGGAAGAGATCCAGCGGTGTTTGAGGGCCCCATAAGGAGTACCATG
AGGAAGCCCAGAAGTGGGACCGCTACACTGACCTGTACCCAGCCCTCGGCCTGGCTCGTGCAATTAACAAGTGGC
ATCGGCGCCACGGCTACACCAGCTCCCTGGAGTACCCGACAACATCCTCAACTTCGTCAAGAAGCACCCGCTGA
TGGAGAGCAGTGGGGCCTCGGTGGAGCCGCCCTGCTCGTGAAGAAGGGCACCAACTTCACCCACCTGGTGG
CCGACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGCTGTTTATTGGCACAGGTGAGGATGGCTGCTCA
AGGCTGTGAGCTGGGGCCTGGGTTCACCTGATTGAGGAGCTGCAGCTGTTTGACAGGAGCCCATGAGAAGT
TGGTGTATCTCAGTGCAGAAAGCTGCTTTTGGCGGCTCCCGCTCTCAGCTGGTGCAGTGCCTGGTGGCCGACT
GCATGAAGTATCGCTCCTGTGCAGACTGTGCTCTGCCCCGGGACCCCTATTGCGCCTGGAGCGTCAACACCAGCC
GCTGTGTGGCCGTGGGTGGCCACTCTGGGTCTTCTGTATCCAGCATGTGATGACCTCGGACACTTCAGGCATCT
GCAACCTCCGTGGCAGTAAGAAAGTCAGGCCCACTCCCAAAAACATCACGGTGGTGGCGGGCACAGACCTGGTGC
TGCCCTGCCACCTCTCTCCAACCTGGCCCATGCCCGCTGGACCTTTGGGGGCCGGGACCTGCCTGCCGAACAGC
CGGGTCTCTTCCCTACGATGCCCGGCTCCAGGCCCTGGTTGTGATGGCTGCCAGCCCCCATGCCGGGGCT
ACCACTGCTTTTCAGAGGAGCAGGGGGCGCGGTGGCTGCTGAAGGCTACCTTGTGGCTGTCTGGCAGGCCCGT
CGGTGACCTTGGAGGCCCGGGCCCCCTGGAACCTGGGGCTGGTGTGGCTGGCGGTGGTGGCCCTGGGGGCTG

TGTGCGCTGGTGTCTGCTGCTGCTGGTGCTGTGTCATTGCGCGCGCGGCTGCGGGAAGAGCTGGAGAAAGGGGCCAAGG
CTACTGAGAGGACCTTGGTGTACCCCTGGAGCTGCCAAGGAGCCACCAGTCCCCCTTCCGGCCCTGTCTGT
AACCAGATGAGAAACTTTGGGATCCTGTGCGTTACTACTATTTCAGATGGCTCCCTTAAGATAGTACCTGGGCGATG
CCCGGTGCCAGCCCGGTGGGGGGCCCCCTTCGCCACCTCCAGGCATCCCAGGCCAGCCTCTGCCTTCTCCAAC
GGCTTCACTTGGGGGTGGCGGAAGTCAAATGCCAATGGTTACGTGCGCTTACAATAGGAGGGGAGGACCGGG
GAGGGCTCGGGGACCCCTCTGAGCTCGCGGATGAATGAGACGCAACTTGCAGCAACGCCAGGCACCTCGCCCG
ACTCCAACCCCGAGGAGTCATCAGTATGAGGGGAACCCCCACCGCGTCGGCGGGAAGCGTGGGAGGTGTAGCTCC
TACTTTTGCACAGGCACCAGTATCTCAGGGACATGGCACGGGCACCTGCTCTGTCTGGGACAGATACTGCCAG
CACCACCCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACCTGCCACTTGGTGTGGCTCACCAGGGCACCGAG
CTCGCAGAAGGCATCTTCCCTCTCTCTGTGAATCACAGACACCGGGACCCAGCGGCCCAAACTTTTCAAGGCA
GAAGTTTCAAGATGTGTGTTGTCTGTTATTTGCACATGTGTTGTGTGTGTGTATGTGTGTGTGCACGGCGCT
GCGCGCTTGTGGCATAGCTTCTGTTTCTGTCAAGTCTTCCCTTGGCTGGGTCTCTCTGGTGTGATGTCATTGGAGC
TATGAAGGGGAAGGGGTGCTATCACTTTGTCTCTCCTACCCCCACTGCCCGAGGTGTGGGCAGCGATGTACATA
TGGAGGTGGGGTGGACAGGGTGTCTGTGCCCTTTCAGAGGGAGTGCAGGGCTTGGGGTGGGCCTAGTCTGTCTCT
AGGGCTGTGAATGTTTTCAGGGTGGGGGGAGGGAGATGAGCCTCCTGTGTGTTTGGGGGGAAGGGTGGGTGGGG
CTTCCCACCTTGGCCCCGGGGTTAGTGGTATTTTATACTTGGCTTCTTCTGTACAGGGCTGGGAAAGGCTGTGT
GAGGGGAGAGAAGGAGAGGGTGGGCTGTGTGGACAATGCTTACCTACTCTTTCAGCCCTAGGAGGAGGGCTCC
TAACAGTGTAACTATTGTGTGCCCGGTATTTATTTGTTGTAAATTTGAGTATTTTATATTGACAAATAAA
ATGGAGAAAAA

The MOL5a protein encoded by SEQ ID NO:13 has 833 amino acid residues and is presented using the one-letter code in Table 5B. The Psort profile for MOL5a predicts that this sequence is likely to be localized at the mitochondrial inner membrane with a certainty of 0.8000 or plasma membrane with a certainty of 0.7000. MOL5a has a cleavage site between amino acids 20 and 21 (GIG-AE), and a molecular weight of 92617.0 Daltons.

Table 5B. Encoded MOL5a protein sequence (SEQ ID NO:14)

MAPHWAVWLLAARLWGLGIGAEVWNVLVPRKTVSSGELATVVRRFSQTGIQDFLTLTLTEPTGLLYVGAREAL
FAFSVEALELQGAISWEAPVEKKTECIQKGKNNQTECFNFIREFLPYNASHLYVCGTYAFQPKCTYVNMILTFT
LEHGEFEDGKGKCPYDPAKGHAGLLVDGELYSATLNNFLGTETPIILRNMGPHHSMKTEYLAFWLNEPHFVGS
YVPELSVGSFTGDQDDKVYFLFRERAVESDQYAEQVVARVARVCKDGGARLTKRWKTTFLKARLACSAPNWQL
YFNQLQAMHTLQDTSWHTNFTFGVFOAQWGDMYLSAICHEYQLEBTVFEGPYKEYHEEAQKWDRYTDVPVSP
RPGSCINNWHRRHGYTSSLELPDNTLNFVKHPLMBEQVGRWSRPLLVKKGNTFNTHLVADRVTGLGDATYTV
LFIGTGQANLLKAVSLGPVWHLIEELQLFDQEPMSRLVLSQSQKLLFAGSRSQLVQLPVADCMKYRSCADCVL
ARDPYCAWSVNTSRCVAVGGHSGSFLIQHVMTSDTSGICNLRGSKKVRPTPKNITVVAGTDLVLPCHLSSNLA
HARWTFGGRLPAEQGSFLYDARLQALVMAAQPRHAGAYHCFSEEQGARLAAEGYLVAVVAGPSVTLBARA
PLENLGLVWLAVVALGAVCLVLLLLVLSLRRLREELEKGAKATERTLVYPLELPKEPTSPFFRPCPEPDEKL
WDPFGVYYSDGSLKIVPGHARCQPGGPPSPPPGIPGQPLPSPTRLHLGGGRNSNANGYVRLQLGGEDRGGLG
HLPELADELRRKLQORQPLPDSNPESSV

The disclosed nucleic acid sequence for MOL5a has 2917 of 3443 bases (84%)
10 identical to a semaphorin 4C mRNA (GENBANK-ID: S79463|acc:S79463) (E= 0.0).

The full MOL5a amino acid sequence has 729 of 834 amino acid residues (87%) identical to, and 772 of 834 residues (92%) positives with, the 834 amino acid semaphorin 4C Precursor protein from *Mus musculus* (Mouse) (ptnr:SPTREMBL-ACC: Q64151) (E= 0.0). In addition, this protein contains the following protein domains (as defined by Interpro) at the indicated nucleotide positions: Sema domain (a.a. 53-481; IPR001627), integrin_B (a.a. 505-519; IPR000413), Plexin repeat (a.a. 499-551; IPR002165), ig (a.a. 570-629; IPR000353)

MOL5a expression in different tissues was examined through TaqMan as described below in Example 1.

Chromosomal Localization

MOL5a has been localized to human chromosome 2.

MOL5b

Another disclosed novel semaphorin 4C -like nucleic acid of 2558 nucleotides, MOL5b, (also referred to as SC14998905_EXT) is shown in Table 5C. An ORF begins with an ATG initiation codon at nucleotides 21 - 23 and ends with a TGA codon at nucleotides 2520-2522. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 5C, and the start and stop codons are in bold letters.

Table 5C. MOL5b Nucleotide Sequence (SEQ ID NO:15)

TCAGAGCCGGGGCGTGCGCCATGGCCCCACACTGGGCTGTCTGGCTGTGGCAGCAAGGCTGTGGGGCTGGGCA
TTGGGGCTGAGGTGTGGTGAACCTTGTGCCGCGTAAGACAGTGTCTTCTGGGGAGCTGGCCACGGTAGTACGGC
GGTTCTCCAGACCGGCATCCAGGACTTCTGACACTGACGCTGACGGAGCCCACTGGGCTTCTGTACGTGGGCG
CCAGGGACCATGCCTCTGCACTGGGCGTCCCTGTGTCTGTGCTGCAAGGCTGTGATCTCCTGGGAGGCCCCCGTGG
AGAAGAAGACTGAGTGTATCCAGAAAGGAAGAACAACAGACCGAGTGCTTCAACTTCATCCGCTTCTGTCAGC
CCTACAATGCCCTCCACCTGTACGTCTGTGGCACCTACGCCTTCCAGCCCAAGTGCACCTACGTCAACATGCTCA
CCTTCACTTTGGAGCATGGAGAGTTGAAGATGGGAAGGGCAAGTGTCCCTATGACCCAGCTAAGGGCCATGCTG
GCCTTCTGTGGATGGTGAAGTGTACTCGGCCACACTCAACAACCTTCTGGGCACGGAACCCATTATCCTGCGTA
ACATGGGGCCCCACCACTCCATGAAGACAGAGTACCTGGCCTTTTGGCTCAACGAACCTCACTTTGTAGGCTCTG
CCTATGTACCTGAGAGTGTGGGACGCTTACCGGGGACGACGACAAGGTCTACTTCTTCTTCAGGGAGCGGGCAG
TGGAGTCCGACTGCTATGCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTCTGCAAGGGCGATATGGGGGGCGCAC
GGACCTGCAAGGAAGTGGACACGTTCTGAAGGCGCGGCTGGCATGCTCTGCCCCGAACCTGGCAGCTCTACT
TCAACCAGCTGCAAGGCGATGCACACCTGCAAGACACCTCTGGCACAACACCACTTCTTTGGGGTTTTCAG
CACAGTGGGGTGACATGTACCTGTGCGGCATCTGTGAGTACCACTTGAAGAGATCCAGCGGGTGTGAGGGGCC
CCTATAAGGAGTACCATGAGGAAGCCAGAAAGTGGGACCGCTACACTGACCTGTACCCAGCCCTCGGCCTGGCT
CGTGCAATTAACAACCTGGCATCGGCGCCACGGCTACACCACTCCCTGGAGCTACCCGACAACATCCTCAACTTCG
TCAAGAAGCACCCGCTGATGGAGGAGCAGGTGGGGCTCGGTGGAGCCGCCCCCTGCTCGTGAAGAAGGGCACCA
ACTTCAACCCACCTGGTGGCCGACCGGGTTACAGGACTTGATGGAGCCACCTATACAGTGTCTGTTTATTGGCACAG
GAGACGGCTGGCTGTCTAAGGCTGTGAGCCTGGGGCCCTGGGTTTCACTGATGAGGAGCTGCAGCTGTTTGACC
AGGAGCCCATGAGAAGCCTGGTGTCTCTCAGAGCAAGAAGCTGTCTTTGCGGCTCCCGCTCTCAGCTGGTGC
AGCTGCCCGTGGCCGACTGCATGAAGTATCGCTCTGTGCAGACTGTGTCTCGCCCCGGGACCCCTATTGCGCCT
GGAGCGTCAACACCAGCCGCTGTGTGGCCGTGGGTGGCCACTCTGGATCTCTACTGATCCAGCATGTGATGACCT
CGGACACTTCAGGCATCTGCAACCTCCGTGGCAGTAAGAAAGTCAAGGCCACTCCCAAAAACATCACGGTGGTGG
CGGCAACAGACCTGGTGTGCTGCCCTGCCACCTCTCTCAACTTGGCCCATGCCCGCTGGACCTTTGGGGGCCGGG
ACCTGCCTGCGGAACAGCCCGGGTCTTCTCTACGATGCCCGGCTCCAGGCCCTGGTTGTGATGGCTGCCAGC
CCCGCATGCCGGGGCTTACCACTGCTTTTCAAGAGGAGCAGGGGGCGGGCTGGCTGTGAAGGCTACCTTGTGG
CTGTGCTGGCAGGCCCCGTGGTGACCTTGGAGGCCCGGGCCCCCTGGAAAACCTGGGGCTGGTGTGGCTGGCGG
TGGTGGCCCTGGGGGCTGTGTGCTGGTGTGCTGCTGCTGGTGTGCTCATTTGCGCGGCGGCTGCGGGAAGAGC
TGGAGAAAGGGGCCAAGGCTACTGAGAGGACCTTGGTGTACCCCTGGAGCTGCCAAGGAGCCACCACTGCCCC
CCTTCCGGCCCTGTCTGTAACAGATGAGAACTTTGGGATCCTGTGCGTTACTACTATTAGATGGCTCCCTTA
AGATAGTACCTGGGCATGCCCGGTGCCAGCCCGGTGGGGGGCCCCCTTCGCCACCTCCAGGCATCCAGGCCAGC
CTCTGCCCTTCTCAACTCGGCTTCACTGGGGGGTGGGGGCGAACTCAAATGCCAATGGTTACGTGCGCTTACAAC
TAGGAGGGGAGGACCGGGGAGGGCTCGGGCACCCCTGCCTGAGCTCGCGGATGAAGTGAAGACGCAAACTGCAGC
AACGCCAGCCACTGCCGACTCAACCCCGAGGAGTCATCAGTATGAGGGGAACCCCCACCGCTCGGCGGGAAG
CGTGGGAG

The MOL5b protein encoded by SEQ ID NO:16 has 833 amino acid residues and is presented using the one-letter code in Table 5D. The Psort profile for MOL5b predicts that this sequence is likely to be localized at the plasma membrane with a certainty of 0.7000.

Table 5D. Encoded MOL5b protein sequence (SEQ ID NO:16)

MAPHWAVWLLAARLWGLGIGAEVWNLVPRKTVSSGELATVVRFSQTGIQDFLTLTLTEPTGLLYVGARDHA

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SALGVPVLLQLQAVISWEAPVEKKTECIQKGKNNQTECFNFI RFLQPYNASHLYVCGTYAFQPKCTYVNMLTFT
LEHGEFEDGKGKCPYDPAKGHAGLLVDGELYSATLNNFLGTEPIILRNMGPHHSMKTEYLAFWLNPHFVGS
YVPESVGSFTGDDDKVYFFFRERAVESDCYAEQVVARVARVCKGDMGGARTLQRKWTTFLLKARLACSA
PNWQLYFNQLQAMHTLQDTSWHNTTFFGVFQAQWGDMYLSAICEYQLEEIQRVFEFGPYKEYHEEAQKWD
RYTDPVPSRPGSCINNWHRRHGYTSSLELPDNI LN FVKKHPLMEEQVGP RWSRPLL VKKGTNFTHLVAD
RVTGLDGATYTVLFIGTGDGWLKAVSLGPWVHLIEELQLFDQEPMRSLVLSQS KLLFAGSRSQLVQLP
VADCMKYRSCADCVLARDPYCAWSVNTSRCVAVGGHSGSLLIQHVMTSDTSGICNLRGSKKVRPTPKNI
TVVAGTDLVLPCHLSSNLAHARWTFGGRDLPABQPGSFLYDARLQALVVMQAQPRHAGAYHCFSEEQ
GARLAAEGYLVAVVAGPSVTLEARA PLENLGLVWLAVVALGAVCLVLLLLVLSLRRRLREELEKGAKAT
ERTLVYPLELPKEPTSPFFRCPPEPDBKLWDPVGYYS DSGSLKIVPGHARCQPGGGPPSPPGIPGQPLPSPT
RLHLGGGRNSNANGYVRLQLGGEDRGGLGHPLPELADELRRKLQORQPLPDSNPRESSV

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The disclosed nucleic acid sequence for MOL5b has 1695 of 2019 bases (83%) identical to a mouse Semaphorin4C mRNA (GENBANK-ID: S79463) (E= 0.0).

5 The full MOL5b amino acid sequence has 722 of 834 amino acid residues (86%) identical to, and 765 of 834 residues (91%) positive with the amino acid Semaphorin4C HOMOLOG protein from *Mouse* (S79463_ SEMA_4C_MOUSE) (E= 0.0). The global sequence homology (as defined by FASTA alignment with the full length sequence of this protein) is 91 % amino acid homology and 86 % amino acid identity.

Chromosomal Localization

10 MOL5b has been localized to human chromosome 2.

MOL5c

In the present invention, the target sequence identified previously, MOL5b, was subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most
 15 downstream sequence available for the reverse primer. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on *in silico* predictions for the full length cDNA, part (one or more exons) of the DNA or protein
 20 sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences sequences from other species. These primers were then employed in PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney,
 25 lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus. Usually the resulting amplicons were gel purified, cloned and sequenced to high redundancy. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and

ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported below, which is designated MOL5c (Accession Number CG50907-02).

5 This differs from the previously identified sequence, MOL5b, in having 17 different amino acids.

The disclosed novel semaphorin 4C -like nucleic acid of 3112 nucleotides, MOL5c, (also referred to as CG50907-02) is shown in Table 5E. An ORF begins with an ATG initiation codon at nucleotides 104 - 106 and ends with a TGA codon at nucleotides 2603-

10 2605. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 5E, and the start and stop codons are in bold letters.

Table 5E. MOL5c Nucleotide Sequence (SEO ID NO:17)

TGCTGCGGGCCCTCTGGTTTGCTTTCTCTGGCTGTGATTCTGACCATGTCTTTCCCTCAGCAGGACAGCTGG
CCTGAAGCTCAGAGCGGGGCGTGCGCCATGGCCCCACACTGGGCTGTCTGGCTGCTGGCAGCAAGGCTGTGGGG
CCTGGGCATTGGGGCTGAGTGTGGTGGAACTTGTGCCCGTAAGACAGTGTCTTCTGGGGAGCTGGCCACGGT
AGTACGCGCGGTCTCCCAAGCCGGCATCCAGGACTCTCTGACATCGAGCTGACGGAGCCCCACTGGGCTCTGTGA
CTGGGGCGTCCAGGAGCATGCTCTGCACTGGGCGTCCCTGTGTGTCTGCTGCAGGCTGTGATCTCTGGGAGGC
CCCCGTGGAGAAGAAGACTGAGTGTATCCAGAAAGGGAAGAACACCAGACAGGAGTGCTTCAACTTTCATCCGCTT
CCTGCAGCCCTACAATGCCTCCACCTGTACGTCTGTGGCACCTACGCCCTTCCAGCCCAAGTGCACCTACGTCAA
CATGCTCACCTTCACTTTGGAGCATGGAGAGTTTGAAGATGGGAAGGGCAAGTGTCCCTATGACCCAGCTAAGGG
CCATGCTGGCCCTTCTGTGGATGGTGAGCTGTACTCGGCCACACTCAACAACCTTCTGGGCACGGAACCCATTAT
CTCGCTGAATCATGGGGCCCCACCACTCCATGAAGACAGAGTACCTGGCCCTTTGGGCTCAACGAACCTCACTTGT
AGGCTCTGCCTATGTACCTGAGAGTGTGGGCAGCTTACGGGGGACGACGACAAGGCTTACTTCTTCTCAGGGA
GCGGGCAGTGGAGTCCGACTGCTATGCCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTCTGCAAGGGCGATATGGG
GGGCGCACGGACCTTCAGAGGAAGTGGACACGTTCTTGAAGGCGCGGCTGGCATGCTCTGCCCGAAGCTGGCA
GCTCTACTTCAACAGGCTGCAGGCGATGACACACCTCTGCAGGACACCTCTGGCACAACACCACTTCTTTGGGGT
TTTTCAAGCACAGTGGGGTGAGCTGACCTCTCGGCCATCTGTGAGTACCACTTGGAAAGAGATCAGCGGGTGT
TGAGGGCCCCATAAGGAGTACCATGAGGAAGCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCTCG
GCCTGGCTCGTGCATTAACTGGCATCGGCGCCACGGCTACACCAAGCTCCCTGGAGCTACCCGACAACATCCT
CAACTTCGTCAGAAGCACCCGCTGATGGAGGAGCAGTGGGGGCTCGGTGGAGCCGCCCTCTGCTCGTGAAGAA
GGGACCAACTTCAACCACTGGTGGCCGAGCCGGGTTCAGGACTTGATGGAGCCCACTATACAGTGTGTTTAT
TGGCACAGGAGACCGCTGGCTGCTCAAGGCTGTGAGCTTGGGGCTCGGGTTCACTGATGAGAGTCTGCAGCT
GTTTGACCAGGAGCCCATGAGAAGCTGGTGCATCTCAGAGCAAGAAGCTGCTCTTTGCCGGCTCCCGCTCTCA
GCTGGTGAGCTGCCCGTGGCCGACTGCATGAAGTATCGTCTCTGTGCAGACTGTGTCTCGCCGGGACCCCTA
TGCGCCTGGAGCGTCAACACCAAGCCGCTGTGTGGCCGTGGGTGGCCACTCTGGATCTCTACTGATCCAGCATGT
GATGACCTCGGACACTTCAGGCATCTGCAACTCCGTGGCAGTAAGAAGTCAGGCCCACTCCCAAACATCAC
GGTGGTGCGGGGCACAGACTCTGGTGTGCCCTCGCACTCTCTTCAACTTGGCCCATGCCCGCTGGACCTTTGG
GGGCGGGACCTGCCTGCGGAACAGCCCGGGTCTCTCTACGATGCCCGGCTCCAGGCCCTGGTTGTGATGGC
TGCCAGCCCCGCCATGCCGGGGCCTACCACTGCTTTTCAAGGAGCAGGGGGCGCGGTGGCTGCTGAAGGCTA
CCTTGTGGTCTGCTGTGGCAGGCGCGTGGTGACCTTGGAGGCCCGGGCCCCCTGGAAAAACCTGGGGCTGTGTGT
CTGGCGGTGTGTGGCCCTGGGGCTGTGTGCTCTGGTGTGCTGTGCTGTGCTGTGCTGCTGCTGCTGCTGCTG
GGAAGAGCTGGAGAAAGGGGCAAGGCTACTGAGAGGACCTTGGTGTACCCCTGGAGCTGCCAAGGAGCCCA
CAGTCCCCCTTCCGGCCCTGTCTGAAACAGATGAGAACTTTGGGATCCTGTGCGTTACTACTATTACAGATGG
CTCCCTTAAAGATAGTACCTGGGCATGCCCGGTGCCAGCCCGTGGGGGGCCCCCTTCGCCACCTCCAGGCATCCC
AGGCACAGCTCTGCCTTCTCCAATCGGCTTCACTTGGGGGTGGCGGAATCAAATGCCAATGGTTACTGTGCG
CTTACAACATAGGAGGGAGAACCGGGAGGCTCGGGACCCCTCGCTGAGCTGACGGATGAATGAGAGCGAA
ACTGACGCAACGCCAGGCACCTGCCCCGACTCCAACCCGAGGAGTCATCAGTATGAGGGGAACCCCAAGCCGCTCG
GCGGGAAGCGTGGGAGGTGTAGCTCCTACTTTTGACAGGCACCAGCTACCTCAGGGACATGGCACGGGCACCTG
CTCTGTCTGGGACAGATACTGCCAGCACCCACCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACCTGCCAC
TGGTGTGGCTCACCAGGCGCACAGCCTCGCAGGAAGGCATCTTCTCTCTCTGTGTAATCACAGACCGCGGGAC
CCGAGCGCCAAACTTTTCAAGGCAGAAGTTCAAGATGTGTTTGTCTGTATTGTGCATGTGTTTGTGTGTG
GTGTGTATGTGTGTGTGCACGCGCGTGCAGCTTGTGGCATAGCCTTCTGTGTTCTGTCAAGTCTTCTCTTGGC

TGGGTCCTCCTGGTGAGTCATTGGAGCTATGAAGGGGAAGGGGTCGTATCACTTTGTCTCTCTACCCCCACTGC
 CCCGAGTGTGGGCAGCGATGTACATATGGAGGTGGG

The MOL5c protein encoded by SEQ ID NO:17 has 833 amino acid residues and is presented using the one-letter code in Table 5F. The Psort profile for MOL5c predicts that this sequence has a signal peptide and the signal peptide is predicted by SignalP to be cleaved between amino acid 20 and 21: GIG-AE. This sequence is likely to be localized at the mitochondrial inner membrane with a certainty of 0.8000 and the plasma membrane with a certainty of 0.7000.

Table 5F. Encoded MOL5c protein sequence (SEQ ID NO:18)

MAPHWAVWLLAARLWGLGIGAEVWVNLVPRKTVSSGELATVVRFSQTGIQDFLTTLTLEPTGLLYVGARDHA
 SALGVPVLLQLQAVISWEAPVEKKTECIQKGKNNQTECFNFIREFLOPYNASHLYVCGTYAFQPKCTYVNMLTFT
 LEHGEFEDGKGCPCYDPAKGHAGLLVDGELYSATLNNFLGTPEIILRNMGPHHSMKTEYLAPWLNPHFVGS
 YVPESVGSFTGDDDKVYFFFRERAVESDCYAEQVVARVARVCKGDMGGARTLQRKWTTFLLKARLACSAPNWQL
 YFNQLQAMHTLQDTSWHNTTFPGVFQAQWGDMYLSAICEYQLBEEIQRVFEGPYKEYHEEAQKWDRTDVPVSP
 RPGSCINWHRHRYTSSLELPDNIINLVKHHPLMEEQVGPWRSRPLLVKKGNTNTHLVADRVTLGLDGATYTV
 LFIGTGDGWLKAVSLGPVWHLEELQLFDQEPMSLVLSQSKLLFAGSRSQLVQLPVADCMKYRSCADCVL
 ARDPYCAWSVNTSRCAVAGGHSGSLLIQHVMTSDTSGICNLRGSKKVRPTPKNITVVAGTDLVLPCHLSSNLA
 HARWTFGGRDLPAEQPGSFLYDARLQALVMAAQPRHAGAYHCFSEEQARLAAEGYLVAVVAGPSVTLEARA
 PLENLGLVWLAVVALGAVCLVLLLLVLSLRRLRREELEKGAKATERTLVYPLELPKEPTSPFPRPCPEPDEKL
 WDFVGYYSYDGSLSKIVPGHARCQPGGPPSPPPGIPGQPLPSPTRLHLGGGRNSNANGYVRIQLGGEDRGGLG
 HPLPELADELRRKLQQRQPLPDSNPPESSV

The disclosed nucleic acid sequence for MOL5c has 2879 of 2906 bases (99%) identical to a gb:GENBANK-ID:AB051526|acc:AB051526.1 mRNA from *Homo sapiens* (*Homo sapiens* mRNA for KIAA1739 protein, partial cds) (E= 0.0).

The full MOL5 amino acid sequence has 722 of 834 amino acid residues (86%) identical to, and 765 of 834 amino acid residues (91%) similar to, the 834 amino acid residue ptmr:SWISSPROT-ACC:Q64151 protein from *Mus musculus* (Mouse) (SEMAPHORIN 4C PRECURSOR (SEMAPHORIN I) (SEMA I) (SEMAPHORIN C-LIKE 1) (M-SEMA F)) (E= 0.0). The global sequence homology (as defined by FASTA alignment with the full length sequence of this protein) is 91% amino acid homology and 86% amino acid identity.

The presence of identifiable domains in the protein disclosed herein was determined by searches versus domain databases such as Pfam, PROSITE, ProDom, Blocks or Prints and then identified by the Interpro domain accession number. Significant domains are summarized in Table 5G.

Table 5G: Domain similarities for MOL5c

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
-----	-----	-----	-----	---

Sema	Sema domain	664.4	5.8e-196	1
Plexin_repeat	Plexin repeat	25.8	0.001	1
ig	Immunoglobulin domain	8.5	0.44	1
integrin_B	Integrins, beta chain	7.0	0.04	1

5 Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
-----	-----	-----	-----	-----	-----	-----	-----
Sema	1/1	53	481 ..	1	490 []	664.4	5.8e-196
10 integrin_B	1/1	505	519 ..	1	14 []	7.0	0.04
Plexin_repeat	1/1	499	551 ..	1	67 []	25.8	0.001
ig	1/1	570	629 ..	1	45 []	8.5	0.44

The Sema domain occurs in semaphorins, which are a large family of secreted and
 15 transmembrane proteins, some of which function as repellent signals during axon guidance.
 Sema domains also occur in a hepatocyte growth factor receptor, in SEX protein (Goodman et
 al., 1998, Cell 95: 903-916) and in viral proteins.

The presence of these domains indicates that MOL5c likely has properties similar to
 those of other proteins known to contain this/these domain(s) and similar to the properties of
 20 these domains.

Chromosomal Localization

MOL5c maps to chromosome 2. This assignment was made using mapping
 information associated with genomic clones, public genes and ESTs sharing sequence identity
 with the disclosed sequence and CuraGen Corporation's Electronic Northern bioinformatic
 25 tool.

Tissue Expression

MOL5c is expressed in at least the following tissues: adrenal gland, bone marrow,
 brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain -
 thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney,
 30 lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary
 gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea and
 uterus. Expression information was derived from the tissue sources of the sequences that were
 included in the derivation of the sequence of MOL5c.

35 MOL5a also has homology to other proteins as shown in BLAST alignment results in
 Table 5H.

Table 5H. BLAST results for MOL5a						
Gene Index/ Identifier		Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 12698023 dbj BAB 21830.1 (AB051526)		KIAA1739 protein [Homo sapiens]	963	785/801 (98%)	789/801 (98%)	0.0

gi 8134699 sp Q64151 SM4C_MOUSE	SEMAPHORIN 4C PRECURSOR (SEMAPHORIN I) (SEMA I) (SEMAPHORIN C-LIKE 1) (M-SEMA F)	834	722/834 (86%)	765/834 (91%)	0.0
gi 13637386 ref XP_002614.2	hypothetical protein FLJ20369 [Homo sapiens]	510	510/510 (100%)	510/510 (100%)	0.0
gi 8923346 ref NP_060259.1	sema domain, immunoglobulin domain (Ig), transmembrane domain TM; cytokeratin 14; adipocyte-derived leucine aminopeptidase; hypothetical protein MGC10851; hypothetical protein FLJ14662; sphingomyelin phosphodiesterase -1, acid lysosomal; Pro-platelet ba>	510	509/510 (99%)	509/510 (99%)	0.0
gi 13633937 sp Q9NTN9 SM4G_HUMAN	SEMAPHORIN 4G PRECURSOR	838	292/673 (43%)	381/673 (56%)	e-138

This information is presented graphically in the multiple sequence alignment given in Table 5I (with MOL5a being shown on line 1, and MOL5b on line 2) as a ClustalW analysis comparing MOL5 with related protein sequences.

5

Table 5I Information for the ClustalW proteins:

- 1) MOL5a (SEQ ID NO:14)
- 2) MOL5b (SEQ ID NO:16)
- 3) gi|12698023|dbj|BAB21830.1| (AB051526) KIAA1739 protein [Homo sapiens] (SEQ ID NO:46)
- 4) gi|8134699|sp|Q64151|SM4C_MOUSE SEMAPHORIN 4C PRECURSOR (SEMAPHORIN I) (SEMA I) (SEMAPHORIN C-LIKE 1) (M-SEMA F) (SEQ ID NO:47)
- 5) gi|8923346|ref|NP_060259.1| sema domain, immunoglobulin domain (Ig), transmembrane domain TM; cytokeratin 14; adipocyte-derived leucine aminopeptidase; hypothetical protein MGC10851; hypothetical protein FLJ14662; sphingomyelin phosphodiesterase-1, acid lysosomal; Pro-platelet ba> (SEQ ID NO:48)
- 6) gi|13633937|sp|Q9NTN9|SM4G_HUMAN SEMAPHORIN 4G PRECURSOR (SEQ ID NO:49)

20

	10	20	30	40
MOL5a			
MOL5b	-----			
gi 12698023	LCSHLWQPGLGSCWSEGFPEAGSTHSRLCLLLCWTLEAV			
gi 8134699	-----			
gi 13637386	-----			
gi 8923346	-----			
gi 13633937	-----			

		50	60	70	80
MOL5a				
MOL5b		-----			
gi 12698023	GSRAKKRAAAERAKVGVGCPALRPEVPLTLRARAIISLMAS				
gi 8134699	-----				
gi 13637386	-----				
gi 8923346	-----				
gi 13633937	-----				
		90	100	110	120
MOL5a				
MOL5b		-----			
gi 12698023	SGRKLWLRYPSFLPAAWICLLPGWERLGRPRWGCQGRLF				
gi 8134699	-----				
gi 13637386	-----				
gi 8923346	-----				
gi 13633937	-----				
		130	140	150	160
MOL5a	MAPHWAVWLLAARLWGLGIGAEVWNNLVPRKTVSS				
MOL5b	MAPHWAVWLLAARLWGLGIGAEVWNNLVPRKTVSS				
gi 12698023	QKCPALPIRGFGWHLVAVGAGSRGARLRVPEQGSQPSA				
gi 8134699	MAPHWAVWLLAAGLWGLGIGAEVWNNLVPRKTVSS				
gi 13637386	-----				
gi 8923346	-----				
gi 13633937	MWGRLEPIILLSLTATAVPGPSLRRPSRELDATP				
		170	180	190	200
MOL5a	GELATVVRFRFSQTGIDFLTLTLEPTGLLYVGAR				
MOL5b	GELATVVRFRFSQTGIDFLTLTLEPTGLLYVGAR				
gi 12698023	AMLTPAELATVVRFRFSQTGIDFLTLTLEPTGLLYVGAR				
gi 8134699	GELVTVVRFRFSQTGIDFLTLTLEPTGLLYVGAR				
gi 13637386	-----				
gi 8923346	-----				
gi 13633937	RMTIPYELSGTRHFKG-QAONYSTULLLEASARLLVGAR				
		210	220	230	240
MOL5a	EALFAPSVEAL--ELQGAISWEAPVEKKTECIQKGKNNQT				
MOL5b	DHASALGVFVL--LLOAVISWEAPVEKKTECIQKGKNNQT				
gi 12698023	EALFAPSMEAL--ELQGAISWEAPVEKKTECIQKGKNNQT				
gi 8134699	EALFAPSVEAL--ELQGAISWEAPVEKKTECIQKGKNNQT				
gi 13637386	-----				
gi 8923346	-----				
gi 13633937	GALFSLSANDIGDGAHKETWEASPEMOSKCHOKGKNNQT				
		250	260	270	280
MOL5a	ECFNFIRFLQPYNASHLYVCGTYAFQPKCTYVNNLTFTLE				
MOL5b	ECFNFIRFLQPYNASHLYVCGTYAFQPKCTYVNNLTFTLE				
gi 12698023	ECFNFIRFLQPYNASHLYVCGTYAFQPKCTYVNNLTFTLE				
gi 8134699	ECFNFIRFLQPYNSHLYVCGTYAFQPKCTYVNNLTFTLD				
gi 13637386	-----				
gi 8923346	-----				
gi 13633937	ECFNFIRFLQRLNSTHLYACGTRAFQPLCAATDAAFTIP				
		290	300	310	320
MOL5a	HGEFEDGKGKCPYDPAKGHAGLLVDGELYSATLNNFLGTE				
MOL5b	HGEFEDGKGKCPYDPAKGHAGLLVDGELYSATLNNFLGTE				
gi 12698023	HGEFEDGKGKCPYDPAKGHAGLLVDGELYSATLNNFLGTE				
gi 8134699	RAEFEDGKGKCPYDPAKGHTGLLVDGELYSATLNNFLGTE				
gi 13637386	-----				
gi 8923346	-----				
gi 13633937	-TSFEEGKEKCPYDPAKGFGLLIDGGLYATRYEER-SI				

	330	340	350	360
MOL5a	PIILRNMGPHHSKTEYLAFWLN	EPHFVGSAYVPESVGSF		
MOL5b	PIILRNMGPHHSKTEYLAFWLN	EPHFVGSAYVPESVGSF		
gi 12698023	PIILRNMGPHHSKTEYLAFWLN	EPHFVGSAYVPESVGSF		
gi 8134699	PIILRNMGTHHSKTEYLAFWLN	EPHFVGSAYVPESVGSF		
gi 13637386	-----	-----	-----	-----
gi 8923346	-----	-----	-----	-----
gi 13633937	PDIRRSRPHSLRTEETPMHNL	DAEFVFSVLVRESKASA		
	370	380	390	400
MOL5a	TGDDDKVYELFRERAVES	-----	DCYAEQVVARVARVCK	
MOL5b	TGDDDKVYFFFRERAVES	-----	DCYAEQVVARVARVCK	
gi 12698023	TGDDDKVYFFFRERAVES	-----	DCYAEQVVARVARVCK	
gi 8134699	TGDDDKVYFFFRERAVES	-----	DCYAEQVVARVARVCK	
gi 13637386	TGDDDKVYFFFRERAVES	-----	DCYAEQVVARVARVCK	
gi 8923346	-----	-----	-----	-----
gi 13633937	VGDDDKVYFFFRERATEEGSG	SFTQSRSSSHRVARVARVCK		
	410	420	430	440
MOL5a	GDMGCARTLQKKWTFLLKARL	ACSAPNWOLYFNQLQAMHT		
MOL5b	GDMGCARTLQKKWTFLLKARL	ACSAPNWOLYFNQLQAMHT		
gi 12698023	GDMGCARTLQKKWTFLLKARL	ACSAPNWOLYFNQLQAMHT		
gi 8134699	GDMGCARTLQKKWTFLLKARL	VCSAPNWOLYFNQLQAMHT		
gi 13637386	-----	-----	-----	-----
gi 8923346	-----	-----	-----	-----
gi 13633937	GDLGGKGLLQKKWTFLLKARL	ICHIP-----LLETTRGVCS		
	450	460	470	480
MOL5a	LQDTSWHNTTFFGVFOA	---QWGD	MYLSAICEYQLEEIQRV	
MOL5b	LQDTSWHNTTFFGVFOA	---QWGD	MYLSAICEYQLEEIQRV	
gi 12698023	LQDTSWHNTTFFGVFOA	---QWGD	MYLSAICEYQLEEIQRV	
gi 8134699	LQDTSWHNTTFFGVFOA	---QWGD	MYLSAICEYQLEEIQRV	
gi 13637386	LQDTSWHNTTFFGVFOA	---QWGD	MYLSAICEYQLEEIQRV	
gi 8923346	-----	-----	-----	-----
gi 13633937	MDAETSSRTTEFYAETLSTQ	NKTLKASAI	CRYDLAEIQAV	
	490	500	510	520
MOL5a	FEGPYKEYHEEAQKWD	RYTDPVPS	PRPGSCINNWHRRHGY	
MOL5b	FEGPYKEYHEEAQKWD	RYTDPVPS	PRPGSCINNWHRRHGY	
gi 12698023	FEGPYKEYHEEAQKWD	RYTDPVPS	PRPGSCINNWHRRHGY	
gi 8134699	FEGPYKEYHEEAQKWD	RYTDPVPS	PRPGSCINNWHRRHGY	
gi 13637386	FEGPYKEYHEEAQKWD	RYTDPVPS	PRPGSCINNWHRRHGY	
gi 8923346	FEGPYKEYHEEAQKWD	RYTDPVPS	PRPGSCINNWHRRHGY	
gi 13633937	FEGPYKEYHEEAQKWD	RYTDPVPS	PRPGSCINNWHRRHGY	
	530	540	550	560
MOL5a	TSSLELPDNILNFVKKHPL	MEEQVGPRWSRPLL	VKKGTNF	
MOL5b	TSSLELPDNILNFVKKHPL	MEEQVGPRWSRPLL	VKKGTNF	
gi 12698023	TSSLELPDNILNFVKKHPL	MEEQVGPRWSRPLL	VKKGTNF	
gi 8134699	TSSLELPDNILNFVKKHPL	MEEQVGPRWSRPLL	VKKGTNF	
gi 13637386	TSSLELPDNILNFVKKHPL	MEEQVGPRWSRPLL	VKKGTNF	
gi 8923346	TSSLELPDNILNFVKKHPL	MEEQVGPRWSRPLL	VKKGTNF	
gi 13633937	NSSQPLPSIYLDVFKHPL	MRPVVPTGRGPLL	TKENIRK	
	570	580	590	600
MOL5a	THLVADRVTGLDGATYTV	LFITGQAWLLKAVSL	GFVWHL	
MOL5b	THLVADRVTGLDGATYTV	LFITGQAWLLKAVSL	GFVWHL	
gi 12698023	THLVADRVTGLDGATYTV	LFITGQAWLLKAVSL	GFVWHL	
gi 8134699	THLVADRVTGLDGATYTV	LFITGQAWLLKAVSL	GFVWHL	
gi 13637386	THLVADRVTGLDGATYTV	LFITGQAWLLKAVSL	GFVWHL	
gi 8923346	THLVADRVTGLDGATYTV	LFITGQAWLLKAVSL	GFVWHL	

gi 13633937	THLTGTPVITPAGFTYDILLETCTADGKTHKAVVLCSGMHII
	610 620 630 640
MOL5a	IEELQLFDQ-EPMRSLVLSQS SK LLFAGSRSQLVQLPVAD
MOL5b	IEELQLFDQ-EPMRSLVLSQS SK LLFAGSRSQLVQLPVAD
gi 12698023	IEELQLFDQ-EPMRSLVLSQS SK LLFAGSRSQLVQLPVAD
gi 8134699	VEELQVFDQ-EPV ES SLVLSQS SK KVLFAGSRSQLVQLPVAD
gi 13637386	IEELQLFDQ-EPMRSLVLSQS SK LLFAGSRSQLVQLPVAD
gi 8923346	IEELQLFDQ-EPMRSLVLSQS SK LLFAGSRSQLVQLPVAD
gi 13633937	IEETQVFRSSQSVENLVISLLOHSLVLCAPSGVITQLPSS
	650 660 670 680
MOL5a	CMKYRSCADCVLARDPYCAWSVNTSRCAVAG-GHSGSFLI
MOL5b	CMKYRSCADCVLARDPYCAWSVNTSRCAVAG-GHSGSLLI
gi 12698023	CMKYRSCADCVLARDPYCAWSVNTSRCAVAG-GHSGSLLI
gi 8134699	CMKYRSCADCVLARDPYCAWSVNTSRCAVAG-GHSGSFLI
gi 13637386	CMKYRSCADCVLARDPYCAWSVNTSRCAVAG-GHSGSLLI
gi 8923346	CMKYRSCADCVLARDPYCAWSVNTSRCAVAG-GHSGSLLI
gi 13633937	CSRYRSCVDCVLARDPYCGNDPGTHACALATTIANRTALI
	690 700 710 720
MOL5a	QHVMTSDTSGICNLRGSKKVRPTPKNITVVAGTDLVLPCH
MOL5b	QHVMTSDTSGICNLRGSKKVRPTPKNITVVAGTDLVLPCH
gi 12698023	QHVMTSDTSGICNLRGSKKVRPTPKNITVVAGTDLVLPCH
gi 8134699	QHVANTDTSKMCN QY GHKKVR SI PKNITVVSGTDLVLPCH
gi 13637386	QHVMTSDTSGICNLRGSKKVRPTPKNITVVAGTDLVLPCH
gi 8923346	QHVMTSDTSGICNLRGSKKVRPTPKNITVVAGTDLVLPCH
gi 13633937	QD HERG NRG--C ESS RD TG PP PL KTR SV LRGDDVLLPCD
	730 740 750 760
MOL5a	LSSNLAHARWTFGGRDLPAEQPGSFLYDARLQALVVMAAQ
MOL5b	LSSNLAHARWTFGGRDLPAEQPGSFLYDARLQALVVMAAQ
gi 12698023	LSSNLAHARWTFGGRDLPAEQPGSFLYDARLQALVVMAAQ
gi 8134699	LSSNLAHARWTFG SD DLPAEQPGSFLYD TG LQALVVMAAQ
gi 13637386	LSSNLAHARWTFGGRDLPAEQPGSFLYDARLQALVVMAAQ
gi 8923346	LSSNLAHARWTFGGRDLPAEQPGSFLYDARLQALVVMAAQ
gi 13633937	QFSNLARALWLLNGSMGL SD GG--GVRVGYDGLIVTDAQ
	770 780 790 800
MOL5a	PRHAGAYHCFSEEQGARLAAEGYLVAVVAGP-----SV
MOL5b	PRHAGAYHCFSEEQGARLAAEGYLVAVVAGP-----SV
gi 12698023	PRHAGAYHCFSEEQGARLAAEGYLVAVVAGP-----SV
gi 8134699	SRHSGPYRCYSEEQGTRLAAE SY LVAVVAGS-----SV
gi 13637386	PRHAGAYHCFSEEQGARLAAEGYLVAVVAGP-----SV
gi 8923346	PRHAGAYHCFSEEQGARLAAEGYLVAVVAGP-----SV
gi 13633937	PEHSGNMG CYA ENGLR TL LASYS LT VRPATPAPAPKAPA
	810 820 830 840
MOL5a	TLEARAPLENLGLVWLAVVALGAVCLVLLLLVLSLRRRLR
MOL5b	TLEARAPLENLGLVWLAVVALGAVCLVLLLLVLSLRRRLR
gi 12698023	TLEARAPLENLGLVWLAVVALGAVCLVLLLLVLSLRRRLR
gi 8134699	TLEARAPLENLGLVWLAVVALGAVCLVLLLLVLSLRRRLR
gi 13637386	TLEARAPLENLGLVWLAVVALGAVCLVLLLLVLSLRRRLR
gi 8923346	TLEARAPLENLGLVWLAVVALGAVCLVLLLLVLSLRRRLR
gi 13633937	TPGAQLAP IV RL IV VLATAALGGICL TL ASSI IV MAC-LR
	850 860 870 880
MOL5a	EELEKGAKATERTLVYPLELPKEPTSPFFRCPCEPDEKLW
MOL5b	EELEKGAKATERTLVYPLELPKEPTSPFFRCPCEPDEKLW
gi 12698023	EELEKGAKATERTLVYPLELPKEPTSPFFRCPCEPDEKLW
gi 8134699	EELEKGAKA S ERTLVYPLELPKEP AS PPFRCP EP DEKLW
gi 13637386	EELEKGAKATERTLVYPLELPKEPTSPFFRCPCEPDEKLW

gi 8923346	EELKGAKATERTLVYPLELPKEPTSPFFRCPPEPEKILW
gi 13633937	EGRRGRRLKYSILGRASRAGGSAYQLQTVSGCCPGERDEGD
	890 900 910 920
MOL5a	DPVGYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPLP
MOL5b	DPVGYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPLP
gi 12698023	DPVGYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPLP
gi 8134699	DPVGYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPLP
gi 13637386	DPVGYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPLP
gi 8923346	DPVGYYSYSDGSLKIVPGHARCQPGGGPPSPPPGIPGQPLP
gi 13633937	DEGAGGLEGSCLTIPGEG---APAPFPFPFPFPFPAE-T
	930 940 950 960
MOL5a	SPTRLHLGGGRNSNANGYVRLQLGGEDRGGLGHPLPELAD
MOL5b	SPTRLHLGGGRNSNANGYVRLQLGGEDRGGLGHPLPELAD
gi 12698023	SPTRLHLGGGRNSNANGYVRLQLGGEDRGGLGHPLPELAD
gi 8134699	SPTRLHLGGGRNSNANGYVRLQLGGEDRGGLGHPLPELAD
gi 13637386	SPTRLHLGGGRNSNANGYVRLQLGGEDRGGLGHPLPELAD
gi 8923346	SPTRLHLGGGRNSNANGYVRLQLGGEDRGGLGHPLPELAD
gi 13633937	NGLVALPSRLRRMGNSSVLLKQSNN---GYPAGPCSTFAE
	970 980
MOL5a	ELRRKLQQR-QPLPDSNPEESSV
MOL5b	ELRRKLQQR-QPLPDSNPEESSV
gi 12698023	ELRRKLQQR-QPLPDSNPEESSV
gi 8134699	ELRRKLQQR-QPLPDSNPEESSV
gi 13637386	ELRRKLQQR-QPLPDSNPEESSV
gi 8923346	ELRRKLQQR-QPLPDSNPEESSV
gi 13633937	ELSRILEKRRKHTQLVEQLDESSV

MOL5b and MOL5c share close homology to each other and therefore to other proteins as is shown in the BLAST alignment in Table 5J.

Table 5J. BLAST alignment between MOL5b and MOL5c

5	10 20 30 40 50
MOL5b
MOL5c	TGCTGCGGGCCCCCTCGGTTTGCTTTCTCTGGCTGTGATTCTGACCATG
10	60 70 80 90 100
MOL5b
MOL5c	TCCTTTTCCTCAGCAGGACAGCTGGCCCTGAAGCTCAGAGCCGGGGCGTGC
15	110 120 130 140 150
MOL5b	GCCATGGCCCCACACTGGGCTGTCTGGCTGCTGGCAGCAAGGCTGTGGGG
MOL5c	GCCATGGCCCCACACTGGGCTGTCTGGCTGCTGGCAGCAAGGCTGTGGGG
20	160 170 180 190 200
MOL5b	CCTGGGCATTGGGGCTGAGGTGTGGTGGAACTTGTGCCGCGTAAGACAG
MOL5c	CCTGGGCATTGGGGCTGAGGTGTGGTGGAACTTGTGCCGCGTAAGACAG
25	210 220 230 240 250
MOL5b	TGTCTTCTGGGGAGCTGGCCACGCTAGTACGGCGGTTCTCCAGACCGGC
MOL5c	TGTCTTCTGGGGAGCTGGCCACGCTAGTACGGCGGTTCTCCAGACCGGC
30	260 270 280 290 300
MOL5b	ATCCAGGACTTCCTGACACTGACGCTGACGGAGCCCACTGGGCTTCTGTA

	MOL5c	ATCCAGGACTTCCTGACACTGACGCTGACGGAGCCCACTGGGCTTCTGTA
		310 320 330 340 350
5	MOL5b	GGTGGGCGCCAGGGACCATGCCTCTGCACTGGGCGTCCCTGTGTTGCTGC
	MOL5c	CGTGGGCGCCAGGGACCATGCCTCTGCACTGGGCGTCCCTGTGTTGCTGC
		360 370 380 390 400
10	MOL5b	TGCAGGCTGTGATCTCCTGGGAGGCCCGTGGAGAAGAAGACTGAGTGT
	MOL5c	TGCAGGCTGTGATCTCCTGGGAGGCCCGTGGAGAAGAAGACTGAGTGT
		410 420 430 440 450
15	MOL5b	ATCCAGAAAGGGAAGAACAACAGACCGAGTGCTTCAACTTCATCCGCTT
	MOL5c	ATCCAGAAAGGGAAGAACAACAGACCGAGTGCTTCAACTTCATCCGCTT
		460 470 480 490 500
20	MOL5b	CCTGCAGCCCTACAATGCCTCCACCTGTACGTCTGTGGCACCTACGCCT
	MOL5c	CCTGCAGCCCTACAATGCCTCCACCTGTACGTCTGTGGCACCTACGCCT
		510 520 530 540 550
25	MOL5b	TCCAGCCCAAGTGCACCTACGTCAACATGCTCACCTTCACCTTGGAGCAT
	MOL5c	TCCAGCCCAAGTGCACCTACGTCAACATGCTCACCTTCACCTTGGAGCAT
		560 570 580 590 600
30	MOL5b	GGAGAGTTTGAAGATGGGAAGGGCAAGTGTCCTATGACCCAGCTAAGGG
	MOL5c	GGAGAGTTTGAAGATGGGAAGGGCAAGTGTCCTATGACCCAGCTAAGGG
		610 620 630 640 650
35	MOL5b	CCATGTCTGGCCTTCTTGTGATGGTGAGCTGTACTCGGCCACACTCAACA
	MOL5c	CCATGTCTGGCCTTCTTGTGATGGTGAGCTGTACTCGGCCACACTCAACA
		660 670 680 690 700
40	MOL5b	ACTTCCTGGGCACGGAACCCATTATCCTGCGTAACATGGGGCCCCACCAC
	MOL5c	ACTTCCTGGGCACGGAACCCATTATCCTGCGTAACATGGGGCCCCACCAC
		710 720 730 740 750
45	MOL5b	TCCATGAAGACAGAGTACCTGGCCTTTTGGCTCAACGAACCTCACTTGT
	MOL5c	TCCATGAAGACAGAGTACCTGGCCTTTTGGCTCAACGAACCTCACTTGT
		760 770 780 790 800
50	MOL5b	AGGCTCTGCCTATGTACCTGAGAGTGTGGGCAGCTTCACGGGGACGACG
	MOL5c	AGGCTCTGCCTATGTACCTGAGAGTGTGGGCAGCTTCACGGGGACGACG
		810 820 830 840 850
55	MOL5b	ACAAGGTCTACTTCTTCTCAGGGAGCGGGCAGTGGAGTCCGACTGCTAT
	MOL5c	ACAAGGTCTACTTCTTCTCAGGGAGCGGGCAGTGGAGTCCGACTGCTAT
		860 870 880 890 900
60	MOL5b	GCCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTCTGCAAGGGCGATATGGG
	MOL5c	GCCGAGCAGGTGGTGGCTCGTGTGGCCCGTGTCTGCAAGGGCGATATGGG
		910 920 930 940 950
65	MOL5b	GGGCGCACGGACCTGCAGAGGAAGTGGACCACGTTCTTGAAGGCGCGGC
	MOL5c	GGGCGCACGGACCTGCAGAGGAAGTGGACCACGTTCTTGAAGGCGCGGC
		960 970 980 990 1000
70	MOL5b	TGGCATGCTCTGCCCCGAACCTGGCAGCTCTACTTCAACCAGCTGCAGGCG

MOL5c TGGCATGCTCTGCCCCGAAGTGGCAGCTCTACTTCAACCAGCTGCAGGGCG

5
MOL5b ATGCACACCCCTGCAGGACACCTCCTGGCACAACACCACCTTCTTTGGGGT
MOL5c ATGCACACCCCTGCAGGACACCTCCTGGCACAACACCACCTTCTTTGGGGT

10
MOL5b TTTTCAAGCACAGTGGGGTGACATGTACCTGTGGCCATCTGTGAGTACC
MOL5c TTTTCAAGCACAGTGGGGTGACATGTACCTGTGGCCATCTGTGAGTACC

15
MOL5b AGTTGGAAGAGATCCAGCGGGTGTTCAGGGCCCCCTATAAGGAGTACCAT
MOL5c AGTTGGAAGAGATCCAGCGGGTGTTCAGGGCCCCCTATAAGGAGTACCAT

20
MOL5b GAGGAAGCCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCTCG
MOL5c GAGGAAGCCCAGAAGTGGGACCGCTACACTGACCCTGTACCCAGCCCTCG

25
MOL5b GCCTGGCTCGTGCATTAACAACCTGGCATCGGCGCCACGGCTACACCAGCT
MOL5c GCCTGGCTCGTGCATTAACAACCTGGCATCGGCGCCACGGCTACACCAGCT

30
MOL5b CCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAGAAGCACCCGCTG
MOL5c CCCTGGAGCTACCCGACAACATCCTCAACTTCGTCAAGAAGCACCCGCTG

35
MOL5b ATGGAGGAGCAGGTGGGGCCTCGGTGGAGCCGCCCTGCTCGTGAAGAA
MOL5c ATGGAGGAGCAGGTGGGGCCTCGGTGGAGCCGCCCTGCTCGTGAAGAA

40
MOL5b GGGCACCACCTTCACCCACCTGGTGGCCGACCGGGTTACAGGACTTGATG
MOL5c GGGCACCACCTTCACCCACCTGGTGGCCGACCGGGTTACAGGACTTGATG

45
MOL5b GAGCCACCTATACAGTGCTGTTTCATTGGCACAGGAGACGGCTGGCTGCTC
MOL5c GAGCCACCTATACAGTGCTGTTTCATTGGCACAGGAGACGGCTGGCTGCTC

50
MOL5b AAGGCTGTGAGCCTGGGGCCCTGGGTTTCACCTGATTGAGGAGCTGCAGCT
MOL5c AAGGCTGTGAGCCTGGGGCCCTGGGTTTCACCTGATTGAGGAGCTGCAGCT

55
MOL5b GTTTGACCAGGAGCCCATGAGAAGCCTGGTGCTATCTCAGAGCAAGAAGC
MOL5c GTTTGACCAGGAGCCCATGAGAAGCCTGGTGCTATCTCAGAGCAAGAAGC

60
MOL5b TGCTCTTTGCGCGCTCCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCCGAC
MOL5c TGCTCTTTGCGCGCTCCCGCTCTCAGCTGGTGCAGCTGCCCGTGGCCGAC

65
MOL5b TGCATGAAGTATCGCTCCTGTGCAGACTGTGTCTCGCCCGGGACCCCTA
MOL5c TGCATGAAGTATCGCTCCTGTGCAGACTGTGTCTCGCCCGGGACCCCTA

70
MOL5b TTGCGCCTGGAGCGTCAACACCAGCCGCTGTGTGGCCGTGGGTGGCCACT

	MOL5c	TTGCGCCTGGAGCGTCAACACCAGCCGCTGTGTGGCCGTGGGTGGCCACT
	
		1710 1720 1730 1740 1750
5	MOL5b	CTGGATCTCTACTGATCCAGCATGTGATGACCTCGGACACTTCAGGCATC
	MOL5c	CTGGATCTCTACTGATCCAGCATGTGATGACCTCGGACACTTCAGGCATC
	
		1760 1770 1780 1790 1800
10	MOL5b	TGCAACCTCCGTGGCAGTAAGAAAGTCAGGCCCACTCCCAAAAACATCAC
	MOL5c	TGCAACCTCCGTGGCAGTAAGAAAGTCAGGCCCACTCCCAAAAACATCAC
	
		1810 1820 1830 1840 1850
15	MOL5b	GGTGGTGGCGGGCACAGACCTGGTGCTGCCCTGCCACCTCTCCTCCAACT
	MOL5c	GGTGGTGGCGGGCACAGACCTGGTGCTGCCCTGCCACCTCTCCTCCAACT
	
		1860 1870 1880 1890 1900
20	MOL5b	TGGCCCATGCCCCGTGGACCTTTGGGGGCGGGACCTGCCTGCGGAACAG
	MOL5c	TGGCCCATGCCCCGTGGACCTTTGGGGGCGGGACCTGCCTGCGGAACAG
	
		1910 1920 1930 1940 1950
25	MOL5b	CCCGGGTCCTTCCTCTACGATGCCCGGCTCCAGGCCCTGGTTGTGATGGC
	MOL5c	CCCGGGTCCTTCCTCTACGATGCCCGGCTCCAGGCCCTGGTTGTGATGGC
	
		1960 1970 1980 1990 2000
30	MOL5b	TGCCCAGCCCCGCGCATGCCGGGGCCTACCACTGCTTTTCAGAGGAGCAGG
	MOL5c	TGCCCAGCCCCGCGCATGCCGGGGCCTACCACTGCTTTTCAGAGGAGCAGG
	
		2010 2020 2030 2040 2050
35	MOL5b	GGCGCGGCTGGCTGCTGAAGGCTACCTTGTGGCTGCTCGTGGCAGGCCCG
	MOL5c	GGCGCGGCTGGCTGCTGAAGGCTACCTTGTGGCTGCTCGTGGCAGGCCCG
	
		2060 2070 2080 2090 2100
40	MOL5b	TCGGTGACCTTGGAGGCCCGGGCCCCCTGGAAAACCTGGGGCTGGTGTG
	MOL5c	TCGGTGACCTTGGAGGCCCGGGCCCCCTGGAAAACCTGGGGCTGGTGTG
	
		2110 2120 2130 2140 2150
45	MOL5b	GCTGGCGGTGGTGGCCCTGGGGGCTGTGTGCCCTGCTGCTGCTGCTGG
	MOL5c	GCTGGCGGTGGTGGCCCTGGGGGCTGTGTGCCCTGCTGCTGCTGCTGG
	
		2160 2170 2180 2190 2200
50	MOL5b	TGCTGTCAATTGCGCCGCGGCTGCGGGAAGAGCTGGAGAAAGGGGCCAAG
	MOL5c	TGCTGTCAATTGCGCCGCGGCTGCGGGAAGAGCTGGAGAAAGGGGCCAAG
	
		2210 2220 2230 2240 2250
55	MOL5b	GCTACTGAGAGGACCTTGGTGTACCCCTGGAGCTGCCCAAGGAGCCAC
	MOL5c	GCTACTGAGAGGACCTTGGTGTACCCCTGGAGCTGCCCAAGGAGCCAC
	
		2260 2270 2280 2290 2300
60	MOL5b	CAGTCCCCCTTCCGGCCCTGTCTGAACCAGATGAGAACTTTGGGATC
	MOL5c	CAGTCCCCCTTCCGGCCCTGTCTGAACCAGATGAGAACTTTGGGATC
	
		2310 2320 2330 2340 2350
65	MOL5b	CTGTGCGTTACTACTATTAGATGGCTCCCTTAAGATAGTACCTGGGCAT
	MOL5c	CTGTGCGTTACTACTATTAGATGGCTCCCTTAAGATAGTACCTGGGCAT
	
		2360 2370 2380 2390 2400
70	MOL5b	GCCTGGTGCCAGCCCGGTGGGGGGCCCCCTTCGCCACCTCCAGGCATCCC

MOL5c **GCCCGGTGCCAGCCCCGGTGGGGGGCCCCCTTCGCCACCTCCAGGCATCCC**
 2410 2420 2430 2440 2450
 5 MOL5b
 MOL5c **AGGCCAGCCTCTGCCTTCTCCAACCTCGGCTTCACTGGGGGCTGGGCGGA**
 2460 2470 2480 2490 2500
 10 MOL5b **ACTCAAATGCCAATGGTTACGTGCGCTTACAACCTAGGAGGGGAGGACCGG**
 MOL5c **ACTCAAATGCCAATGGTTACGTGCGCTTACAACCTAGGAGGGGAGGACCGG**
 2510 2520 2530 2540 2550
 15 MOL5b **GGAGGGGCTCGGGCAGCCCCCTGCCTGAGCTCGCGGATGAACCTGAGACGCAA**
 MOL5c **GGAGGGGCTCGGGCAGCCCCCTGCCTGAGCTCGCGGATGAACCTGAGACGCAA**
 2560 2570 2580 2590 2600
 20 MOL5b **ACTGCAGCAACGCCAGCCACTGCCCGACTCCAACCCCGAGGAGTCATCAG**
 MOL5c **ACTGCAGCAACGCCAGCCACTGCCCGACTCCAACCCCGAGGAGTCATCAG**
 2610 2620 2630 2640 2650
 25 MOL5b
 MOL5c **TATGAGGGGAACCCCCACCGCGTCGGCGGGAAGCGTGGGAGGTGTAGCTC**
 2660 2670 2680 2690 2700
 30 MOL5b
 MOL5c **CTACTTTTGCCAGGCCACCAGCTACCTCAGGGACATGGCACGGGCACCTG**
 2710 2720 2730 2740 2750
 35 MOL5b
 MOL5c **CTCTGTCTGGGACAGATACTGCCCAGCACCACCCGGCCATGAGGACCTG**
 2760 2770 2780 2790 2800
 40 MOL5b
 MOL5c **CTCTGTCTCAGCAGGGGCACTGCCACTTGGTGTGGCTCACCAGGACACCAG**
 2810 2820 2830 2840 2850
 45 MOL5b
 MOL5c **CCTCGCAGAAGGCATCTTCCTCCTCTCTGTGAATCACAGACACGCGGGAC**
 2860 2870 2880 2890 2900
 50 MOL5b
 MOL5c **CCCAGCCGCCAAAACCTTTTCAAGGCAGAAGTTTCAAGATGTGTGTTTGTG**
 2910 2920 2930 2940 2950
 55 MOL5b
 MOL5c **TGTATTTCACATGTGTTTGTGTGTGTGTATGTGTGTGCACGCGCG**
 2960 2970 2980 2990 3000
 60 MOL5b
 MOL5c **TGCGCGCTTGTGGCATAGCCTTCCTGTTTCTGTCAAGTCTTCCCTTGGCC**
 3010 3020 3030 3040 3050
 65 MOL5b
 MOL5c **TGGGTCTCCTCGGTGAGTCATTGGAGCTATGAAGGGGAAGGGGTCGTATC**
 3060 3070 3080 3090 3100
 70 MOL5b

	Pfam pfam01403	-----GPN-SKILP-MRGRVEYPRDQCPNS-----SG-----DL
		410 420 430 440 450
5	MOL5_1	PDNLINLVKRLPLAEQNGERWRERPLKKGTN--FTHIVADRVITGLEGA
	Pfam pfam01403	PDNLINLVKRLPLAEQNGERWRERPLKKGTN--FTHIVADRVITGLEGA
		460 470 480 490 500
10	MOL5_1	TYTVLFTSTGQWLDRAVSLG--PWVHITBELQLE--DOEPMSIVE
	Pfam pfam01403	TYTVLFTSTGQWLDRAVSLG--PWVHITBELQLE--DOEPMSIVE
15	MOL5_1
	Pfam pfam01403	SQSK
		SQKN (SEQ ID NO:97)

Table 5L. Domain Analysis of MOL5

gnl|Smart|smart00409, IG, Immunoglobulin
 CD-Length = 86 residues, only 79.1% aligned
 Score = 42.0 bits (97), Expect = 1e-04

		10 20 30 40 50
20	MOL5_5	SKNLTIVVAGTDLVLPCHLSS--N-LAHARITFG--GRDLPAB
	Smart smart00409	SKNLTIVVAGTDLVLPCHLSS--N-LAHARITFG--GRDLPAB
		60 70 80 90 100
25	MOL5_5	QPG-SFLYDA--RLQAVTMAACERHAGAVHCFSEEQGAR
	Smart smart00409	QPG-SFLYDA--RLQAVTMAACERHAGAVHCFSEEQGAR
		110
30	MOL5_5	LEAGGYLVAVVAGPS
	Smart smart00409	LEAGGYLVAVVAGPS
		SGGSASS-GVTLTVL (SEQ ID NO:98)

The protein similarity information, expression pattern, cellular localization, and map location for MOL5 suggest that this Semaphorin 4C-like protein may have important structural and/or physiological functions characteristic of the Semaphorin family. These functions include growth cone guidance, axonal pathfindin, and embryonic development. Therefore, the MOL5 nucleic acids and proteins are useful in potential diagnostic and therapeutic applications and as a research tool. These include serving as a specific or selective nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These also include potential therapeutic applications such as the following: (i) a protein therapeutic, (ii) a small molecule drug target, (iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a nucleic acid useful in gene therapy (gene delivery/gene ablation), (v) an agent promoting tissue regeneration *in vitro* and *in vivo*, and (vi) a biological defense weapon.

The MOL5 nucleic acids and proteins have applications in the diagnosis and/or treatment of various diseases and disorders. For example, the compositions of the present invention will have efficacy for the treatment of patients suffering from: Rheumatoid arthritis

(RA), CNS disorders, Alzheimer, Down syndrome, Schizophrenia, Parkinsons diseases as well as other diseases, disorders and conditions.

These materials are further useful in the generation of antibodies that bind immuno-specifically to the novel MOL5 substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-MOLX Antibodies" section below. The disclosed MOL5 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated MOL5 epitope is from about amino acids 30 to 70. In another embodiment, a MOL5 epitope is from about amino acids 100 to 150. In additional embodiments, MOL5 epitopes are from about amino acids 175 to 200, 220 to 450, 550 to 575, 590 to 610, and from about amino acids 675 to 850. These novel proteins can also be used to develop assay systems for functional analysis.

MOL6

The disclosed novel kappa casein precursor -like MOL6 nucleic acid of 603 nucleotides (also referred to as GMAC060288_A) is shown in Table 6A. An open reading begins with an ATG initiation codon at nucleotides 31-33 and ends with a TAA codon at nucleotides 574-576. A putative untranslated region upstream from the initiation codon and downstream from the termination codon are underlined in Table 6A, and the start and stop codons are in bold letters.

Table 6A. MOL6 Nucleotide Sequence (SEQ ID NO:19)

<p>TTTTTTTAAATTTATCTTTAGGTGCAATAATGAAGAGTTTCTTCTAGTTGTCAATGCCCTGGCATTAAACCTG CCTTTTGTCTAGTGGAGGTTCAAACCAGAAACAACCAGCATGCCATGAGAATGATGAAGACCATTCTATCAG AAACGTTACATATGTCCCAATGTATTATGTGCAAAATAGCTATCTTTATTATGGACCCAATTTGTACAAACGT AGACCAGCTATAGCATTAAATAATCAATATGGGCTTCGCACATATTATGCAACCCAAGCTGTAGTTAGGGCACAT GCCCCAATTCTCAGCGGCAATACCTGCCAAATAGCCACCACACTGTGGTACGTGCCCCAACCTGCATCCATCA TTTATTGCAATCCCCCAAAGAAAATT CAGGATAAAATAATCATCCCTACCATCAATACCATGCTACTGTTGAA CCTACACCAGCTCCTGCCACTGAACCAACGGTGGACAGTGTAACTCACTCCAGAAGCTTTTTCAGAGTCCATCATC ACGAGCACCCCTGAGACAACCACAGTTGCAGTTACTCCACCTACGGCATAAAACACCAAGGAAATATCAAAGAA CAC</p>
--

The MOL6 protein encoded by SEQ ID NO:20 has 181 amino acid residues, and is presented using the one-letter code in Table 6B (SEQ ID NO:20). The Psort profile for MOL6 predicts that this sequence has a signal peptide and is likely to be localized outside the cell with a certainty of 0.8200. The most likely cleavage site for a peptide is between amino acids

24 and 25: VQN-QK based on the SignalP result. The molecular weight of the MOL6 protein is 20424.3 Daltons.

Table 6B. Encoded MOL6 protein sequence (SEQ ID NO:20).

MKSFLLVNNALATLPFLLEVNQKQKQACHENDERPFYQKTFTTYVPMYYVQNSYLYYGPNNLYKRRPAIALNNQYG
LRTYYATQAVVRAHAQIPQRQYLPNSHHTVVRPNLHPSFIALPPKKIQDKIIPTINTIATVEPTPAPATEPTVD
SVITPEAFSESIITSTPETTTVAVTPPTA

5 The disclosed nucleic acid sequence has 566 of 586 bases (96 %) identical to a *Homo sapiens* kappa casein precursor mRNA (GENBANK-ID: ACC: I29004) (E value = $9.8e^{-116}$).

The full amino acid sequence of MOL6 was found to have 165 of 182 amino acid residues (90%) identical to, and 168 of 182 residues (92%) positive with, the 182 amino acid residue kappa casein precursor protein from *Homo sapiens* (ptnr: SWISSPROT-ACC:P07498) (E value = $3.0e^{-83}$), 165 of 182 amino acid residues (90%) identical to, and 168 of 182 residues (92%) positive with patp:AAR39351 Recombinant human kappa casein - *Homo sapiens* having 182 aa (E value = $3.0e^{-83}$), and 165 of 182 amino acid residues (90%) identical to, and 168 of 182 residues (92%) positive with patp:AAR92150 Human milk kappa-casein having 182 amino acids (E value = $3.0e^{-83}$).

15 The global sequence homology (as defined by FASTA alignment with the full length sequence of this protein) is 92.265 % amino acid homology and 91.160% amino acid identity. In addition, this protein contains the following protein domains (as defined by Interpro) at the indicated nucleotide positions: casein_kappa (IPR000117) at amino acid positions 1 to 181.

20 The full amino acid sequence of MOL6 was found to have homology with several proteins, including those disclosed in the BLASTP data in Table 6C.

Table 6C. BLAST results for MOL6

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 1705606 sp P07498 CASK_HUMAN	KAPPA CASEIN PRECURSOR	182	154/171 (90%)	157/171 (91%)	3e-59
gi 4885161 ref NP_05203.1	casein, kappa [Homo sapiens]	182	153/171 (89%)	156/171 (90%)	9e-59
gi 186655 gb AAA59456.1	kappa-casein [Homo sapiens]	182	153/171 (89%)	156/171 (90%)	6e-55
gi 13633560 ref XP_003538.3	casein, kappa [Homo sapiens]	182	144/171 (84%)	147/171 (85%)	3e-54
gi 2493502 sp P79139 CASK_CAMDR	KAPPA CASEIN PRECURSOR	182	102/178 (57%)	118/178 (65%)	2e-31

This information is presented graphically in the multiple sequence alignment given in Table 6D (with MOL6 being shown on line 1) as a ClustalW analysis comparing MOL6 with related protein sequences.

Table 6D Information for the ClustalW proteins:

- 1) MOL6 (SEQ ID NO:20)
- 2) gi|1705606|sp|P07498|CASK_HUMAN KAPPA CASEIN PRECURSOR (SEQ ID NO:50)
- 3) gi|4885161|ref|NP_005203.1| casein, kappa [Homo sapiens] (SEQ ID NO:51)
- 4) gi|186655|gb|AA59456.1| kappa-casein [Homo sapiens] (SEQ ID NO:52)
- 5) gi|13633560|ref|XP_003538.3| casein, kappa [Homo sapiens] (SEQ ID NO:53)
- 6) gi|2493502|sp|P79139|CASK_CAMDR KAPPA CASEIN PRECURSOR (SEQ ID NO:54)

		10	20	30	40	50
MOL6	
gi 1705606		MKSFLLVNALALTLPFLAVEVQKQKOPACHENDERPFYQKTFTYVPMYY				
gi 4885161		MKSFLLVNALALTLPFLAVEVQKQKOPACHENDERPFYQKTAPYVPMYY				
gi 186655		MKSFLLVNALALTLPFLAVEVQKQKOPACHENDERPFYQKTAPYVPMYY				
gi 13633560		MKSFLLVNALALTLPFLXXXXXXXXXXXXCHENDERPFYQKTAPYVPMYY				
gi 2493502		MKSFLLVNALALTLPFLAVEVQKQKOPACHENDERPFYQKTFTYVPMYY				
		60	70	80	90	100
MOL6	
gi 1705606		VNSYLYYQENLYQRRPAIAINNNPVVPRYYANPAVVRPHAQIPQROYLP				
gi 4885161		VNSYLYYQENLYQRRPAIAINNNPVVPRYYANPAVVRPHAQIPQROYLP				
gi 186655		VNSYLYYQENLYQRRPAIAINNNPVVPRYYANPAVVRPHAQIPQROYLP				
gi 13633560		VNSYLYYQENLYQRRPAIAINNNPVVPRYYANPAVVRPHAQIPQROYLP				
gi 2493502		VNSYLYYQENLYQRRPAIAINNNPVVPRYYANPAVVRPHAQIPQROYLP				
		110	120	130	140	150
MOL6	
gi 1705606		NSHPTTVVRRPNLHPSFIAIPPKKIQDKIIPTINTIATVEPTPAPATEP				
gi 4885161		NSHPTTVVRRPNLHPSFIAIPPKKIQDKIIPTINTIATVEPTPAPATEP				
gi 186655		NSHPTTVVRRPNLHPSFIAIPPKKIQDKIIPTINTIATVEPTPAPATEP				
gi 13633560		NSHPTTVVRRPNLHPSFIAIPPKKIQDKIIPTINTIATVEPTPAPATEP				
gi 2493502		NSHPTTVVRRPNLHPSFIAIPPKKIQDKIIPTINTIATVEPTPAPATEP				
		160	170	180		
MOL6			
gi 1705606		TVDSVVTPEAFSESIIITSTPETTTTAVTPPTA				
gi 4885161		TVDSVVTPEAFSESIIITSTPETTTTAVTPPTA				
gi 186655		TVDSVVTPEAFSESIIITSTPETTTTAVTPPTA				
gi 13633560		TVDSVVTPEAFSESIIITSTPETTTTAVTPPTA				
gi 2493502		TVDSVVTPEAFSESIIITSTPETTTTAVTPPTA				

Table 6E lists the domain description from DOMAIN analysis results against MOL6.

- 15 The region from amino acid residue 1 through 116 (SEQ ID NO:20) most probably ($E = 2e^{-36}$) contains a casein kappa domain found in Kappa casein, aligned here in Table 6E. This indicates that the MOL6 sequence has properties similar to those of other proteins known to contain this domain.

Table 6E. Domain Analysis of MOL6

gnl|Pfam|pfam00997, casein_kappa, Kappa casein
 CD-Length = 181 residues, only 64.6% aligned
 Score = 145 bits (366), Expect = $2e^{-36}$

10 20 30 40 50

```

MOL6      .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Pfam|pfam00997  MKSFLLVVNAALALTLPFLVVEVQNCQOPAGCHENDERPEYQKFTFTVVEFY
                    60      70      80      90     100
MOL6      VONSILYYGPNLKKRRPATA-ENNQGLRTYYATQAVTRAHAQIFCRQYL
Pfam|pfam00997  VLNRKPSYGPYYGRRPAVP-ENNPMPYFYAKFAVERPHACIFQWCVL
                    110     120     130     140     150
MOL6      PH-----SEH-TVVRNPNLHPSFIAIPPKKICDRIIPIINTIATVE
Pfam|pfam00997  PH-----IHPPTVVRHPRPHPSFIAIPPKKICDKTAIPTINTIATVE
                    160     170     180     190
MOL6      PTEAPATEPTVDSVITPEAFSESLIISIPETITVAVTPTA-----
Pfam|pfam00997  PTEVPT-----PEPIVSTVVTPEASEFII-SIPETITVAVTSTAA (SEQ ID NO:99)

```

The above defined information for MOL6 suggests that this kappa casein precursor-like protein may function as a member of a “Kappa Casein Precursor family”. Members of this family is found as a nutritional component of human milk. Therefore, the novel nucleic acids and proteins identified here may be useful in potential therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated below. The potential therapeutic applications for MOL6 include, but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, kappa casein precursor therapy (kappa casein precursor delivery/kappa casein precursor ablation), research tools, tissue reKappa Casein Precursor ration *in vivo* and *in vitro* of all tissues and cell types composing (but not limited to) those defined here.

The MOL6 nucleic acids and proteins are useful in potential therapeutic applications implicated in nutritional deficiencies. It is used as a nutrient supplement in milk based products to provide a substantial improvement of the nutritional and biological value of the formulae, making it closer in similarity to human milk. Kappa casein can also be used as a pharmaceutical and/or other pathologies and disorders. For example, a cDNA encoding the kappa casein precursor-like protein may be useful in kappa casein precursor therapy, and the kappa casein precursor-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from nutritional deficiencies. MOL6, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

These materials are further useful in the generation of antibodies that bind immuno-specifically to the novel MOL6 substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from

hydrophobicity charts, as described in the "Anti-MOLX Antibodies" section below. The disclosed MOL6 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated MOL6 epitope is from about amino acids 30 to 125. In another embodiment, a MOL6 epitope is from about amino acids 140 to 160. These novel proteins can also be used to develop assay systems for functional analysis.

MOL7

A novel nucleic acid encoding a human Rh type B glycoprotein -like-protein MOL7 was identified by TblastN using CuraGen Corporation's sequence file for MOL7 probes or homologs, and run against the Genomic Daily Files made available by GenBank. The disclosed novel MOL7 nucleic acid of 1765 nucleotides (also referred to as AF193808A) is shown in Table 7A. An open reading frame begins with an ATG initiation codon at nucleotides 39-41 and ends with a TAA codon at nucleotides 1383-1385. A putative untranslated region upstream from the initiation codon and downstream from the termination codon are underlined in Table 7A, and the start and stop codons are in bold letters.

Table 7A. MOL7 Nucleotide Sequence (SEQ ID NO:21)

AAAGCCTGCGAGCGCCAGCCGAGATCGCATCCCAACCCATGGCGGGTCTCCTAGCCGCGCGCGGGCCGGCGACTGCG
AGCTTCCCTTGTGTGCTCTTCTCCAGGGCGCACTGCGGCTCCTTTTGTCTGTCTTTGTCCGCTACAACCACAAAA
CCGACGCTGCCCTCTGGCACCAGGAGCAACCACAGTAACGCGGACAATGAATTTTACTTTTCGCTACCCAAGTTTCCAGG
ACGTGCATGCCATGGTCTTCTGTTGGGCTTTGACTTCTCATGGTCTTCTGTCAGCGTTACGGCTTCAGCAGCGTGGGCT
TCACCTTCTCTCGGCCGCTTTGCCCTGCAGTGGTCCACACTGGTCCAGGGCTTTCTCCACTCCTTCCACGGTGGCC
ACATCCATGTTGGCGTGGAGAGCATGATCAATGCTGACTTTGTGCGGGGGCCGTGCTCATCTCCTTTGGTGCCTGCC
TGGGCAAGACCGGGCTTACCAGCTGCTGCTCATGGCCCTTGTGAGGTGGTGTCTGTTTGGCATCAATGAGTTTGTGC
TCCTTCATCTCCTGGGGGTGAGAGTCTGGGGAGGGATTTCTAGGGTTATGTCTAGTACCATGCTGGAGAAGAGCAAGC
ACCGCCAGGGCTCCGTCTACCATTCAGACCTCTTCGCCATGATTGGTGGGACCATCTTCTGTGGATCTTCTGGCCTA
GCTTCAATGCTGCACTCACAGCGCTGGGGGCTGGGCAGCATCGGACGGCCCTCAACACATACTACTCCCTGGCTGCCA
GCACCTTGGCACCTTTGCCCTTGTGAGCCCTTGTAGGGGAAGATGGGAGGCTTGACATGGTAGTCCACATCCAAATG
CAGCGCTGGGCTGGAGGGGTGTGGTGGGGACCTCAAGTGAAATGATGCTGACACCCCTTTGGGGCTTGGCAGCTGGCT
TCTTGGCTGGGACTGTCTCCACGCTGGGGTACAAGTTCTTTCAGCCCCATCCTTGAATCAAAATTCAAAGTCCAAGACA
CATGTGGAGTCCACAACCTCCATGGGATGCCGGGGCTCCTGGGGGCCCTCCTGGGGGTCTTGTGGCTGGACTTGCCA
CCCATGAAGCTTACGGAGATGGGCTGGAGAGTGTGTTTCCACTCATAGCCGAGGGCCAGCGCAGTGCCACGTCACAGG
CCATGCACACAGCTCTTTCGGGCTGTTTGTCACTGATGTTTGCCTCTGTGGGCGGGGGCCCTTGGAGGTGGGCTCCTGC
TGAAGCTACCTTTCTGGACTCCCCCCCCGACTCCCGAGCACTACGAGGACCAAGTTCAGTGGCAGGTGGTGCCTGGCG
AGCATGAGGATAAAGCCCAGAGACCTCTGAGGGTGGAGGAGGAGCAGCACTCAGGCCTAACCCTGCCCAGCCCCCTGAG
AGGACACGCTCCTTTTCGAAGATGCTGACTGGTGTCTACTAGGAAGTCTTTTGTGAGCTCCATTCTCCAGCTGCAA
GAAGGGAGCCATGAGCCAGAAGGAGGCCCTTTCCACAGGCAGCGTCTCCACAGGGAGAGGGGCAACAGGAGGCTGGG
AAATGGTGGGAGTGGGGCCGTAAGTGGGTACAATAGGGGGAACCTCACCAGATGCCCAACCCGACTGCCCTACCAGC
CTGCACATGGGTAGAAGAGGCCAAATTGAGGCACCAAGTGATCCACTGGCCCCACGTACACAGTTACAGTGAAGCC
CAAGCCAGGCCTGGTTGAGGGTGATAACGCCACTGTCTTTAAGGAAA

The MOL7 protein encoded by SEQ ID NO:21 has 448 amino acid residues, and is presented using the one-letter code in Table 7B (SEQ ID NO:22). The SignalP, Psort and/or Hydropathy profile for MOL7 predict that MOL7 has a signal peptide and is likely to be localized at the plasma membrane with a certainty of 0.6400. The SignalP shows a signal sequence is coded for with the most likely cleavage site being between amino acids 27 and 28:

ATA-VL. This is typical of this type of membrane protein. The molecular weight of the MOL7 protein is 48304.3 Daltons.

Table 7B. Encoded MOL7 protein sequence (SEQ ID NO:22).

MAGSPSRAAGRRQLPLLCFLQGATAVLFAVFRYNHKTDAALWHRSNHNSADNEFYFRYPSFQDV
HAMVFGFDLQVFLQRYGFSSVGFLLAALQWSTLVQGFLHSFHGGHIHVGVESMINADFCAG
AVLISFGAVLGKTGPTQLLLMALLEVVLFGINEFVLLHLLGVRVWGGISRVMSSTMLEKSKHRQGSV
YHSDLFAMIGGTIFLWIFWPSFNAALTALGAGQHRTALNTYISLAASTLGTFFALSALVGEDGRDLMV
VHIQNAALAGGVVGTSSSEMMLTPFGALAAGFLAGTVSTLGKFFTPILESFKFVQDTCGVHNLHGM
PGVLGALLGVLVAGLATHEAYGDGLESVFPLIAEGQRSATSQAMHQLFGLFVTLMFASVGGGLGGGL
LLKLPLFDSPPDSQHYEDQVHWQVVPGEHEDKAQRPLRVVEADTQA

5 The nucleic acid sequence of MOL7 was found to have 680 of 815 bases (83 %) identical to a mouse Rh type b glycoprotein mRNA (GENBANK-ID:AF193808|acc:AF193808).

The full amino acid sequence of MOL7 was found to have 363 of 448 amino acid residues (81%) identical to, and 399 of 448 residues (89%) positive with, the 455 amino acid residue mouse RH TYPE B GLYCOPROTEIN (ptnr: SPTREMBL-ACC:Q9QXP1)

10 The full amino acid sequence of MOL7 was found to have homology with several proteins, including those disclosed in the BLASTP data in Table 7C.

Table 7C. BLAST results for MOL7

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 9966891 ref NP_065140.1	Rh type B glycoprotein [Homo sapiens]	458	433/462 (93%)	435/462 (93%)	0.0
gi 14346006 gb AAK15395.1 (AY013268)	Rh type B glycoprotein [Pan troglodytes]	458	429/462 (92%)	431/462 (92%)	0.0
gi 14486159 gb AAK14651.1 (AY013261)	Rh type B glycoprotein [Sus scrofa]	458	384/462 (83%)	409/462 (88%)	0.0
gi 10946710 ref NP_067350.1	Rhesus blood group-associated B glycoprotein; Rh type B glycoprotein [Mus musculus]	455	362/452 (80%)	398/452 (87%)	e-177
gi 14486161 gb AAK14652.1 (AY013262)	Rh type B glycoprotein [Oryctolagus cuniculus]	458	373/462 (80%)	404/462 (86%)	e-176

This information is presented graphically in the multiple sequence alignment given in Table 7D (with MOL7 being shown on line 1) as a ClustalW analysis comparing MOL7 with related protein sequences.

15

Table 7D Information for the ClustalW proteins:

- 1) MOL7 (SEQ ID NO:22)
2) gi|9966891|ref|NP_065140.1| h type B glycoprotein [Homo sapiens] (SEQ ID NO:55)
3) gi|14346006|gb|AAK15395.1| (AY013268) Rh type B glycoprotein [Pan troglodytes] (SEQ ID NO:56)
4) gi|14486159|gb|AAK14651.1| (AY013261) Rh type B glycoprotein [Sus scrofa] (SEQ ID NO:57)
5) gi|10946710|ref|NP_067350.1| Rhesus blood group-associated B glycoprotein; Rh type B glycoprotein [Mus musculus] (SEQ ID NO:58)
6) gi|14486161|gb|AAK14652.1| (AY013262) Rh type B glycoprotein [Oryctolagus cuniculus] (SEQ ID NO:59)

	10	20	30	40	50		
MOL7	MAGSP	SRAAGRR	LQPLLC	FLQGATA	VLFVAVFVRYNHK	TDAA	LWHRSNH
gi 9966891	MAGSP	SRAAGRR	LQPLLC	FLQGATA	VLFVAVFVRYNHK	TDAA	LWHRSNH
gi 14346006	MAGSP	SRAAGRR	LQPLLC	FLQGATA	VLFVAVFVRYNHK	TDAA	LWHRSNH
gi 14486159	MAGSS	RAAGRR	LQPLLC	FLQGATA	VLFVAVFVRYNHK	TDAA	LWHRSNH
gi 10946710	MARVER	---HRR	IVLP	LLCL	FLQGATA	LLFAT	FVRYNHK
gi 14486161	MAKSP	REAV	AGRR	LLPLLC	FLQGATA	LLFAT	FVRVDO
	60	70	80	90	100		
MOL7	SNADNE	FYFRYP	SFQDVH	AMVFVG	FDLNV	FLQRYG	FSSVGF
gi 9966891	SNADNE	FYFRYP	SFQDVH	AMVFVG	FDLNV	FLQRYG	FSSVGF
gi 14346006	SNADNE	FYFRYP	SFQDVH	AMVFVG	FDLNV	FLQRYG	FSSVGF
gi 14486159	SNADNE	FYFRYP	SFQDVH	AMVFVG	FDLNV	FLQRYG	FSSVGF
gi 10946710	SNADNE	FYFRYP	SFQDVH	AMVFVG	FDLNV	FLQRYG	FSSVGF
gi 14486161	SNADNE	FYFRYP	SFQDVH	AMVFVG	FDLNV	FLQRYG	FSSVGF
	110	120	130	140	150		
MOL7	LQWSTL	VQGF	LHSPH	GGHI	HVG	VESMIN	ADFCAG
gi 9966891	LQWSTL	VQGF	LHSPH	GGHI	HVG	VESMIN	ADFCAG
gi 14346006	LQWSTL	VQGF	LHSPH	GGHI	HVG	VESMIN	ADFCAG
gi 14486159	LQWSTL	VQGF	LHSPH	GGHI	HVG	VESMIN	ADFCAG
gi 10946710	LQWSTL	VQGF	LHSPH	GGHI	HVG	VESMIN	ADFCAG
gi 14486161	LQWSTL	VQGF	LHSPH	GGHI	HVG	VESMIN	ADFCAG
	160	170	180	190	200		
MOL7	QLLLM	ALLEV	VLFC	NEFV	LLHLL	GVFV	WCC
gi 9966891	QLLLM	ALLEV	VLFC	NEFV	LLHLL	GVFV	WCC
gi 14346006	QLLLM	ALLEV	VLFC	NEFV	LLHLL	GVFV	WCC
gi 14486159	QLLLM	ALLEV	VLFC	NEFV	LLHLL	GVFV	WCC
gi 10946710	QLLLM	ALLEV	VLFC	NEFV	LLHLL	GVFV	WCC
gi 14486161	QLLLM	ALLEV	VLFC	NEFV	LLHLL	GVFV	WCC
	210	220	230	240	250		
MOL7	SSTMLE	SKSR	QGSV	YHSD	LFANIG	CTIFL	WIFW
gi 9966891	SSTMLE	SKSR	QGSV	YHSD	LFANIG	CTIFL	WIFW
gi 14346006	SSTMLE	SKSR	QGSV	YHSD	LFANIG	CTIFL	WIFW
gi 14486159	SSTMLE	SKSR	QGSV	YHSD	LFANIG	CTIFL	WIFW
gi 10946710	SSTMLE	SKSR	QGSV	YHSD	LFANIG	CTIFL	WIFW
gi 14486161	SSTMLE	SKSR	QGSV	YHSD	LFANIG	CTIFL	WIFW
	260	270	280	290	300		
MOL7	TALNTY	YSLS	ASTL	CTFALS	ALVGE	DGR	LDNV
gi 9966891	TALNTY	YSLS	ASTL	CTFALS	ALVGE	DGR	LDNV
gi 14346006	TALNTY	YSLS	ASTL	CTFALS	ALVGE	DGR	LDNV
gi 14486159	TALNTY	YSLS	ASTL	CTFALS	ALVGE	DGR	LDNV
gi 10946710	TALNTY	YSLS	ASTL	CTFALS	ALVGE	DGR	LDNV
gi 14486161	TALNTY	YSLS	ASTL	CTFALS	ALVGE	DGR	LDNV
	310	320	330	340	350		
MOL7	EMMLT	PPGALA	AGFL	AGT	VSTL	GYKFF	TPILES
gi 9966891	EMMLT	PPGALA	AGFL	AGT	VSTL	GYKFF	TPILES
gi 14346006	EMMLT	PPGALA	AGFL	AGT	VSTL	GYKFF	TPILES
gi 14486159	EMMLT	PPGALA	AGFL	AGT	VSTL	GYKFF	TPILES
gi 10946710	EMMLT	PPGALA	AGFL	AGT	VSTL	GYKFF	TPILES
gi 14486161	EMMLT	PPGALA	AGFL	AGT	VSTL	GYKFF	TPILES
	360	370	380	390	400		
MOL7	EMMLT	PPGALA	AGFL	AGT	VSTL	GYKFF	TPILES
gi 9966891	EMMLT	PPGALA	AGFL	AGT	VSTL	GYKFF	TPILES
gi 14346006	EMMLT	PPGALA	AGFL	AGT	VSTL	GYKFF	TPILES
gi 14486159	EMMLT	PPGALA	AGFL	AGT	VSTL	GYKFF	TPILES
gi 10946710	EMMLT	PPGALA	AGFL	AGT	VSTL	GYKFF	TPILES
gi 14486161	EMMLT	PPGALA	AGFL	AGT	VSTL	GYKFF	TPILES

```

MOL7
gi|9966891|
gi|14346006|
gi|14486159|
gi|10946710|
gi|14486161|

```

410 420 430 440 450

 GVLGALLGVVAGLATHEAYGFGLESVFPLIAEGQRSATSOAHHQLFGLE
 GVLGALLGVLVAGIATHEAYGFGLESVFPLIAEGQRSATSOAHHQLFGLE
 GVLGALLGVLVAGLATHEAYGFGLESVFPLIAEGQRSATSOAHHQLFGLE
 GVLGALLGVVAGLATHEAYGFGLESVFPLIAEGQRSATSOAHHQLFGMF
 GVLGALLGALWISLTITHEAYGFGLESVFPLIAEGQRSATSOAHHQLFGLE

```

MOL7
gi|9966891|
gi|14346006|
gi|14486159|
gi|10946710|
gi|14486161|

```

460

 RPLRVEEADTQA
 RPLRVEEADTQA
 RPLRVEEADTQA
 GSLRPEEADTQA
 RPLRGGSDTQA
 EALRVEEADTQA

Table 7E lists the domain description from DOMAIN analysis results against MOL7. The region from amino acid residue 25 through 336 (SEQ ID NO:22) most probably ($E = 1e^{-33}$) contains an ammonium transporter domain found in Ammonium transporters, aligned here in Table 7E. This indicates that the MOL7 sequence has properties similar to those of other proteins known to contain this domain.

Table 7E. Domain Analysis of MOL7

gnl|Pfam|pfam00909, Ammonium_transp, Ammonium Transporter Family
CD-Length = 395 residues, only 78.7% aligned
Score = 137 bits (345), Expect = 1e-33

Sequence logos for Pfam00909 (MOL7) showing conservation across 350 positions. The logos are arranged in a grid with 10 rows. Each row shows a sequence of amino acids with vertical bars indicating conservation. The sequences are:

Row 1: ATAVLFAVVRKAN-HKTDPAIWHRSNHSNADIEFY--FRVSEFQDVHA--

Row 2: AWILISAALVIVM-QPGFALDE--SGLVRSKIVLIN--ILNKNFQDVAGV

Row 3: MVTVSGHDLNVLQRYGFSVVGFT---FLDAAFACRSITVQGE---

Row 4: LANWGCQGLADGRSY--PSGFIGN---LG-LIAGICRGITPDEL---F

Row 5: FHSHPGCH--THVGLPSMINHFFCAGVLTSEFVLLCKTGTPQRIILMALL

Row 6: PLFQLMFAA-TAIIILISGAVERIKFSAYILLESALLGLTVVPPVAHWVWG

Row 7: S-VVLFGINEFVTV---LHLICVRVAGGILHRVMSSTMLEKSKH

Row 8: E-GGWLAKLGVLV---DFAGSTVHILFCGYAGIARILVIGSPRLG

Row 9: R---RGSVVESDLFAMTGGTITLPLATVPSFNAALT--ELGAGQHR--

Row 10: RFT---KNSAITTEINLEFARLQ--TILLRFGCFGNAGSALADGRARA--

Row 11: TADNTYYSLAST--GTFAFSALVGGDCR--LDVWVHTQNAALAGGVV

Row 12: AAVNTNLRAAGGALTAILISRL--KTKCK--FNN-LGLAAGALAGLMA

5
 10
 15

```

MOL7      VGISSEMMITPEGALAAGFPAGTWTGLGYKF---FTPILESKPRMODTC
Pfam|pfam00909  H-DFACGWSPEGALIIICLPAGVLSVLGYKF---LKE---KLGEEDDPL

          360      370      380      390      400
MOL7      GVNHLGMPGWLCAALGVIVGGATHEAYGDGLSEFPPLTAEQORSATSC
Pfam|pfam00909  DFFVFGVGGHGGTAVGDFEALVY-----TSGHSGGLLYENS---K

          410      420      430      440      450
MOL7      AMHQLFGLFVTMFASVGGGLGCEILLKIPFLDSPPDQHYEDQVHWQVV
Pfam|pfam00909  QLGVLIGIAVETIAYAFETFILGILIGITLG--LRVSEEEFKVGLDVAE

          ....|.
MOL7      PSEHED
Pfam|pfam00909  HSEETAY (SEQ ID NO:100)
  
```

20 TaqMan Data

Example 2 shows a TaqMan expression profile in 41 normal human tissues and 55 human cancer cell lines. The MOL7 gene is expressed in normal tissues, specifically lung, colon, small intestine, and prostate, and is lost in cancer cell lines.

25
 Example 2 also shows replicate TaqMan expression results in tumor tissues that are often matched with normal adjacent tissue (NAT), as defined by the operating surgeon. The results reveal that the MOL7 human Rh type B glycoprotein is overexpressed in kidney tumors compared with their NAT and normal tissues.

Chromosomal localization:

30
 This gene belongs to genomic DNA GenBank AL139130 which maps to chromosome 1.

Tissue expression:

35
 MOL7 has been found to be expressed in Renal clear cell carcinoma by EST analysis. Genbank EST AI310325 has 100% identity with novel Rh type B glycoprotein and was obtained from 2 pooled tumors (clear cell type). Kidney, AI925934 has 100% identity with novel Rh type B glycoprotein and was obtained from Kidney. Fetal spleen R83833 and AI022447 have 96% identity to novel Rh type B glycoprotein and were obtained from Fetal spleen. The tissue expression profile of was also determined by TaqMan.

Uses of the Compositions of the Invention

40
 The expression pattern, map location and protein similarity information for the MOL7 suggest that this gene may function as "an Rh family" member. Therefore, the MOL7 nucleic acids and proteins are useful in potential therapeutic applications implicated in various pathologies /disorders described and/or other pathologies/disorders

Potential therapeutic uses for MOL7 include: Protein therapeutic, Small molecule drug target, Antibody target (Therapeutic, Diagnostic, Drug targeting/Cytotoxic antibody), Diagnostic and/or prognostic marker, Gene therapy (gene delivery/gene ablation), Research tools, Tissue regeneration *in vitro* and *in vivo* (regeneration for all these tissues and cell types composing these tissues and cell types derived from these tissues)

The MOL7 nucleic acids and proteins are useful in potential therapeutic applications implicated in various names of pathologies/disorders described below and/or other pathologies disorders. For example, a cDNA encoding the RH TYPE B GLYCOPROTEIN -like protein may be useful in gene therapy, and the RH TYPE B GLYCOPROTEIN-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from the pathologies described above. The novel nucleic acid encoding MOL7, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

These materials are further useful in the generation of antibodies that bind immunospecifically to the novel MOL7 substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-MOLX Antibodies" section below. The disclosed MOL7 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated MOL7 epitope is from about amino acids 40 to 80. In another embodiment, a MOL7 epitope is from about amino acids 160 to 190. In additional embodiments, MOL7 epitopes are from about amino acids 175 to 225, 235 to 250, 325 to 345, 360 to 380, and from about amino acids 400 to 450. These novel proteins can also be used to develop assay systems for functional analysis.

MOL8

A novel human Noelin-2-like nucleic acid was identified by TblastN using CuraGen Corporation's sequence file. The disclosed novel MOL8 nucleic acid of 1399 nucleotides (also referred to as SC84366578_A) is shown in Table 8A. An open reading frame begins with an ATG initiation codon at nucleotides 14-16 and ends with a TAG codon at nucleotides 1391-1393. A putative untranslated region downstream from the termination codon are underlined in Table 8A, and the start and stop codons are in bold letters.

Table 8A. MOL8 Nucleotide Sequence (SEQ ID NO:23)

```

TGTTTACTTGAAATGCTACAAACCAACACTCTTTTATCCTAAACAGGAGTCTGTGTTTATGTTTCCCTTGG
TTTCCTCAGACTCAGATTAGTCCTAAAGAAGGGTGGCAGGTGTACAGCTCAGCTCAGGATCCTGATGGGCGGTGCA
TTTGCACAGTTGTTGCTCCAGAACAAAACCTGTGTTCCCGGATGCCAAAAGCAGGCAACTTCGCCAACTACTGGA
AAAGGTACAGAACATGTCCAGTCTATTGAAGTCTTAAACTTGAGAACTCAGAGAGATTTCGAATATGTTTAAAA
ATGGAAACCCAAATGAAAGGGCTGAAGGCAAAATTTCCGCAGATTGAAGATGATCGAAAGACACTTATGACCAAGC
ATTTTCAGCAGGAGTTGAAAGAGAAAATGGACGAGCTCCTGCCTTTGATCCCGTGCTGGAACAGTGC AAAACAGA
TGCTAAGTTCATCACCCAGTTCAGGAGGAAATAAGGAATCTGTCTGCTGTCTCACTGGTATT CAGGAGGAAAT
GGTGCTTATGACTACGAGGAACACACCAAGAGTGTGAGCTTGGAACAAGACTTCGTGACTGCATGAAAAAGC
TATGTGGCAAACTGATGAAAATCACAGGCCAGTTACAGTCAAGACATCTGGAACCCGATT TGGTGCTTGGATGAC
AGACCCTTTAGCATCTGAGAAAAACAACAGAGTATGGTACATGGACAGTTATACTAACAATAAAATTGTTCTGTGAA
TACAAATCAATTGCAGACTTGTGCTAGTGGGGCTGAATCAAGGACATACAACCTTCCTTTCAAGTGGGCAGGAAC TA
ACCATGTTGTCTACAATGGCTCACTCTATTTTAAACAAGTATCAGAGTAATATCATCATCAAATACAGCTTTGATAT
GGGAGAGTGTCTGCCCAACGAAGCCTGGAGTATGCTGTTTTCATAATGTTTACCCCTACACATGGGGTGGATT C
TCTGACATCGACCTAATGGCTGATGAAATCGGGCTGTGGGCTGTGTATGCAACTAACCAGAATGCAGGCAATATG
TCATCAGCCAACTTAACCAAGATACCTTGGAGGTGATGAAGAGCTGGAGCACTGGCTACCCCAAGAGAAGTGCAGG
GGAATCTTTTATGATCTGTGGGACACTGTATGTACCAACTCCCCTTAAGTGGAGCCAGGTGTATATTCCCTAT
TCCACCAAAACCTCCACATATGAGTACACAGACATTCCCTTCCATAACCAATACTTTCACATATCCATGCTTGACT
ACAATGCAAGAGATCGAGCTCTCTATGCTTGAACAATGGCCACCAGGTGCTGTTCAATGTCACCCCTTTCCATAT
CATCAAGACAGAGGATGACACATAGGCAAT

```

The MOL8 protein encoded by SEQ ID NO:23 has 459 amino acid residues, and is presented using the one-letter code in Table 8B (SEQ ID NO:24). The SignalP, Psort and/or Hydropathy profile for MOL8 predict that MOL8 has no signal peptide and is likely to be localized at the microbody (peroxisome) with a certainty of 0.5616. The molecular weight of the MOL8 protein is 53275.2 Daltons.

Table 8B. Encoded MOL8 protein sequence (SEQ ID NO:24).

```

MLQNTLFLKQESVFFYVSLWFPQTQISPKEGWQVYSSAQDPDGRICITVVAPEQNLC SRDAKSRQLRQLLEKVQN
MSQSIEVLNLRTRQDFQYVLKMETQMKGLKAKFRQIEDDRKTLMTKHFQQLKEKMDLPLIPVLEQCKTDAKFI
TQPKKEIRNLSAVLTG IQEIGAYDYELHQRVLSLETRLRDCMKLKGKLMKITGPVTVKTSGTRFGAWMTDPLA
SEKNNRVWYMSYTNKIVREYKSIAD FVSGAESRTYNLPFKWAGTNHVYVNGSLYFNKYQSNIIKYSFDMGRVL
AQRSLEYAGFHNVPYTWGGFSDIDLMADEIGLWAVYATNQAGNIVISQLNQDTLEVMSKSWSTGYPKRSAGESFM
ICGTLVYVNTSHLTGAKVYYSYSTKTSTYEYTDIPFHNQYFPHISMLDYNARDRALYAWNNGHQVLFNVTLFHI I KTE
DDT

```

The nucleotide sequence of MOL8 has 889 of 1286 bases (69%) identical to a *Gallus gallus* NOELIN-2 mRNA (GENBANK-ID: AF239804). The full amino acid sequence of the protein of the invention was found to have 288 of 448 amino acid residues (64%) identical to, and 367 of 448 residues (80%) positive with, the 457 amino acid residue NOELIN-2 protein from *Gallus gallus* (Chicken) (ptr:SP TREMBL-ACC: AAF43715), and 439 of 459 amino acid residues (95%) identical to, and 442 of 459 residues (96%) positive with, the 458 amino acid residue patp:AAB74696 Human membrane associated protein MEMAP-2.

The global sequence homology (as defined by FASTA alignment with the full length sequence of this protein) is 74% amino acid homology and 65% amino acid identity. In addition, this protein contains the following protein domain (as defined by Pfam) at the

indicated nucleotide positions: Olfactomedin-like domain (PF02191) at amino acid positions 201 to 451.

The full amino acid sequence of MOL8 was found to have homology with several proteins including those disclosed in the BLASTP data in Table 8C.

5

Table 8C. BLAST results for MOL8					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 3024210 sp Q62609 NOE1_RAT	NOELIN PRECURSOR (NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN) (PANCORTIN) (1B426B)	485	285/431 (66%)	355/431 (82%)	e-172
gi 13124385 sp Q9IAK4 NOE1_CHICK	NOELIN PRECURSOR (NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN) (PANCORTIN)	485	284/431 (65%)	357/431 (81%)	e-171
gi 9506929 ref NP_062371.1	olfactomedin related ER localized protein [Mus musculus]	485	284/431 (65%)	354/431 (81%)	e-171
gi 7248902 gb AAF43715.1 AF239804_1 (AF239804)	NOELIN-2 [Gallus gallus]	457	284/431 (65%),	357/431 (81%)	e-171
gi 2143875 pir I73636	neuronal olfactomedin-related ER localized protein - rat	457	285/431 (66%)	355/431 (82%)	e-171

Homology between MOL8 and other proteins are presented graphically in the multiple sequence alignment given in Table 8D (with MOL8 being shown on line 1) as a ClustalW analysis comparing MOL8 with related protein sequences.

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Table 8D. Information for the ClustalW proteins:

- 1) MOL8 (SEQ ID NO:24)
- 2) gi|3024210|sp|Q62609|NOE1_RAT NOELIN PRECURSOR (NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN) (PANCORTIN) (1B426B) (SEQ ID NO:60)
- 3) gi|13124385|sp|Q9IAK4|NOE1_CHICK NOELIN PRECURSOR (NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN) (PANCORTIN) (SEQ ID NO:61)
- 4) gi|9506929|ref|NP_062371.1| olfactomedin related ER localized protein [Mus musculus] (SEQ ID NO:62)
- 5) gi|7248902|gb|AAF43715.1|AF239804_1 (AF239804) NOELIN-2 [Gallus gallus] (SEQ ID NO:63)
- 6) gi|2143875|pir||I73636 neuronal olfactomedin-related ER localized protein - rat (SEQ ID NO:64)

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	10	20	30	40	50
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MOL8	-MLQNTNTPILKQESVYFV	-----LWFP
gi 3024210	MSVELLKIGVVLSTAMITNWMSTLPSLVGLNTRLSAASGGTLDRSTG	
gi 13124385	MSVELLKIGVVLSTAMITNWMSTLPSLVGLNTRKLSAASGGTLDRSTG	
gi 9506929	MSVELLKIGVVLSTAMITNWMSTLPSLVGLNTRLSAASGGTLDRSTG	
gi 7248902	-MQASKKLTLPFLIMGT	-----ELTQ
gi 2143875	-MQASKKLTLPFLIMGT	-----ELTQ

	60	70	80	90	100
MOL8	QTQISEKEG	QVYSSAQDP	GRGICITVVA	PEONLC	SRDAKSHQLRQLLEK
gi 3024210	VLPTNP	PEESWQVYSSAQD	SEGRGICITVVA	PQQTNC	SRDARTKQLRQLLEK
gi 13124385	VLPTNP	PEESWQVYSSAQD	SEGRGICITVVA	PQQTNC	SRDARTKQLRQLLEK
gi 9506929	VLPTNP	PEESWQVYSSAQD	SEGRGICITVVA	PQQTNC	SRDARTKQLRQLLEK
gi 7248902	VLPTNP	PEESWQVYSSAQD	SEGRGICITVVA	PQQTNC	SRDARTKQLRQLLEK
gi 2143875	VLPTNP	PEESWQVYSSAQD	SEGRGICITVVA	PQQTNC	SRDARTKQLRQLLEK

	110	120	130	140	150
MOL8	VQNMSQSIEVLNLT	QRTD	EQVILKME	QMKGLKAK	FRQIEDDRNTLMTKH
gi 3024210	VQNMSQSIEVLDRRT	QDRLQYVE	KMENQMK	GLESKFRQ	VEESHKQHLARQ
gi 13124385	VQNMSQSIEVLDRRT	QDRLQYVE	KMENQMK	GLESKFRQ	VEESHKQHLARQ
gi 9506929	VQNMSQSIEVLDRRT	QDRLQYVE	KMENQMK	GLESKFRQ	VEESHKQHLARQ
gi 7248902	VQNMSQSIEVLDRRT	QDRLQYVE	KMENQMK	GLESKFRQ	VEESHKQHLARQ
gi 2143875	VQNMSQSIEVLDRRT	QDRLQYVE	KMENQMK	GLESKFRQ	VEESHKQHLARQ

	160	170	180	190	200
MOL8	FGORTAKMDELL	PLIPVLE	QCCTIDAN	FTIQFKEE	IRNLISANLTGQEEI
gi 3024210	FK-AIKAKMDELR	PLIPVLE	EYKADAKL	VLOFKEE	VQNLTSVLNQLQEEI
gi 13124385	FK-AIKAKMDELR	PLIPVLE	EYKADAKL	VLOFKEE	VQNLTSVLNQLQEEI
gi 9506929	FK-AIKAKMDELR	PLIPVLE	EYKADAKL	VLOFKEE	VQNLTSVLNQLQEEI
gi 7248902	FK-AIKAKMDELR	PLIPVLE	EYKADAKL	VLOFKEE	VQNLTSVLNQLQEEI
gi 2143875	FK-AIKAKMDELR	PLIPVLE	EYKADAKL	VLOFKEE	VQNLTSVLNQLQEEI

	210	220	230	240	250
MOL8	GAYDYBELHCEVLS	LEDEL	PLDCMKKL	-CGKLMK	TCGPVTVKTS
gi 3024210	GAYDYBELQSRVSN	LEELRLAC	NQKLACG	KLTCISDP	VTVKTS
gi 13124385	GAYDYBELQSRVSN	LEELRLAC	NQKLACG	KLTCISDP	VTVKTS
gi 9506929	GAYDYBELQSRVSN	LEELRLAC	NQKLACG	KLTCISDP	VTVKTS
gi 7248902	GAYDYBELQSRVSN	LEELRLAC	NQKLACG	KLTCISDP	VTVKTS
gi 2143875	GAYDYBELQSRVSN	LEELRLAC	NQKLACG	KLTCISDP	VTVKTS

	260	270	280	290	300
MOL8	MTDPLASEK	ENRVWYND	SYHNK	IVREYK	SLADFEVGAESRTNL
gi 3024210	MTDPLAPEG	ENRVWYND	SYHNK	RFVREYK	SMVDFMNTDNFTSHRLPHPW
gi 13124385	MTDPLAPEG	ENRVWYND	SYHNK	RFVREYK	SMVDFMNTDNFTSHRLPHPW
gi 9506929	MTDPLAPEG	ENRVWYND	SYHNK	RFVREYK	SMVDFMNTDNFTSHRLPHPW
gi 7248902	MTDPLAPEG	ENRVWYND	SYHNK	RFVREYK	SMVDFMNTDNFTSHRLPHPW
gi 2143875	MTDPLAPEG	ENRVWYND	SYHNK	RFVREYK	SMVDFMNTDNFTSHRLPHPW

	310	320	330	340	350
MOL8	GTNHVYVNGS	LYFNKQ	SHIIIR	FDLKTET	ILKTRSLDYAGYNNMYHYAW
gi 3024210	GTGQVYVNGS	LYFNKQ	SHIIIR	FDLKTET	ILKTRSLDYAGYNNMYHYAW
gi 13124385	GTGQVYVNGS	LYFNKQ	SHIIIR	FDLKTET	ILKTRSLDYAGYNNMYHYAW
gi 9506929	GTGQVYVNGS	LYFNKQ	SHIIIR	FDLKTET	ILKTRSLDYAGYNNMYHYAW
gi 7248902	GTGQVYVNGS	LYFNKQ	SHIIIR	FDLKTET	ILKTRSLDYAGYNNMYHYAW
gi 2143875	GTGQVYVNGS	LYFNKQ	SHIIIR	FDLKTET	ILKTRSLDYAGYNNMYHYAW

	360	370	380	390	400
MOL8	GGHSDIDL	MDENGLW	AVYATN	QNA	GIVISQ
gi 3024210	GGHSDIDL	MDENGLW	AVYATN	QNA	GIVISQ
gi 13124385	GGHSDIDL	MDENGLW	AVYATN	QNA	GIVISQ
gi 9506929	GGHSDIDL	MDENGLW	AVYATN	QNA	GIVISQ
gi 7248902	GGHSDIDL	MDENGLW	AVYATN	QNA	GIVISQ
gi 2143875	GGHSDIDL	MDENGLW	AVYATN	QNA	GIVISQ

	410	420	430	440	450
MOL8	RSAGEAF	IIICGTL	YVTNG	YSGG	TKVHYAYQ
gi 3024210	RSAGEAF	IIICGTL	YVTNG	YSGG	TKVHYAYQ
gi 13124385	RSAGEAF	IIICGTL	YVTNG	YSGG	TKVHYAYQ
gi 9506929	RSAGEAF	IIICGTL	YVTNG	YSGG	TKVHYAYQ
gi 7248902	RSAGEAF	IIICGTL	YVTNG	YSGG	TKVHYAYQ
gi 2143875	RSAGEAF	IIICGTL	YVTNG	YSGG	TKVHYAYQ

		460	470	480
MOL8	
gi 3024210		SMLDYNARDRALYAEINCHGVLRNVTLPHTIETEDDT		
gi 13124385		SMLDYNPKDRALYAMINGHCILYNTLPFHVIRSDEI		
gi 9506929		SMLDYNPKDRALYAMINGHCILYNTLPFHVIRSDEI		
gi 7248902		SMLDYNPKDRALYAMINGHCILYNTLPFHVIRSDEI		
gi 2143875		SMLDYNPKDRALYAMINGHCILYNTLPFHVIRSDEI		

Table 8E lists the domain description from DOMAIN analysis results against MOL8. The region from amino acid residue 201 through 457 (SEQ ID NO:24) most probably (E = 4e⁻⁸⁵) contains a Olfactomedin-like domain, aligned in Table 8E. This indicates that the MOL8 sequence has properties similar to those of other proteins known to contain this domain.

Table 8E. Domain Analysis of MOL8	
gnl Smart smart00284, OLF, Olfactomedin-like domains	
CD-Length = 257 residues, 100.0% aligned	
Score = 308 bits (789), Expect = 4e-85	
	10 20 30 40 50
MOL8	SKIMKIGPVTIRTSGT---RFAAMTDPASE-N-NNRVWYNDSYT
Smart smart00284	GGLAGTSKPVITQTSWK-NAYKSSAAMKQPLNITIK-KSLYWYIPLNI
	60 70 80 90 100
MOL8	-NNKIVREYKSTADSVSAESRTYANLSP-----KWAG-NHVVYNG
Smart smart00284	RVLRSVREYSMSDFQMCKNPTDPLH-----AGCGTGVVVYNG
	110 120 130 140 150
MOL8	SLYFNKYOSMTIKYSFDMGRVLAQRSLEYASTHNVPYTWGGFSDIDIM
Smart smart00284	SLYFNKENSDFICRFDLTTETYOKEPLNGASLNNRPYPYAWGGFSDIDIA
	160 170 180 190 200
MOL8	ADSLGLMAYIATNQAGNIVISQENODTLEAMKSWSTCNPKRSAGEEFMI
Smart smart00284	VDENGLMVIYATEQNAKIVISKLNPAITLTENRTITPKRSASNAEFMI
	210 220 230 240 250
MOL8	CGSLYVINS-----HLTCAKVYVSSTKTSTYEDIDIPFNQYFISM
Smart smart00284	CSILYVIRS-----LGSKCEKVYAYDNTGKEGHLIDIPFNWVEYISM
	260 270
MOL8	LDYNARDRALYAMNNGHGVLRNVTLPFH
Smart smart00284	LDYNPNDRKLYAMNNGHLVHYDIALKP (SEQ ID NO:101)

Uses of the Compositions of the Invention

The above defined information for MOL8 suggests that this Noelin-2-like protein may function as a member of a "Noelin-2 family". This family is involved in neural crest development, and other developmental processes. Therefore, the novel nucleic acids and proteins identified here may be useful in potential therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated below. The potential therapeutic applications for MOL8 include, but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic

and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, tissue regeneration *in vivo* and *in vitro* of all tissues and cell types composing (but not limited to) those defined here.

5 The MOL8 nucleic acids and proteins are useful in potential therapeutic applications implicated in neural crest development in early embryonic stage. For example, a cDNA encoding the Noelin-2-like protein may be useful in gene therapy, and the Noelin-2-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from primary open-angle glaucoma (POAG), and bone disorders, hematopoietic
10 disorders, neuro-developmental disorders, cancer, autoimmune disorders, psychiatric disorders. The novel nucleic acid encoding MOL8, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed.

15 These materials are further useful in the generation of antibodies that bind immuno-specifically to the novel MOL8 substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-MOLX Antibodies" section below. The disclosed MOL8 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated MOL8 epitope is from about amino acids 20
20 to 50. In another embodiment, a MOL8 epitope is from about amino acids 50 to 125. In additional embodiments, MOL8 epitopes are from about amino acids 140 to 210, 225 to 320, 350 to 375, and from about amino acids 380 to 440. These novel proteins can also be used to develop assay systems for functional analysis.

TABLE 9: Summary Of Nucleic Acids And Proteins Of The Invention

Name	Tables	Clone; Description of Homolog	Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO
MOL1	1A, 1B, 1D, 1E	MOL1a: SC29674552_EXT	1	2
		MOL1b: CG56250-02	3	4
MOL2	2A, 2B	MOL2: SC98428706_EXT	5	6
MOL3	3A, 3B 3D, 3E	MOL3a: SC85516573_EXT	7	8
		MOL3b: CG53027-02	9	10
MOL4	4A, 4B,	MOL4: SC_111750277_A	11	12
MOL5	5A, 5B, 5C, 5D, 5E, 5F	MOL5a: SC20422974_A	13	14
		MOL5b: SC14998905_EXT	15	16
		MOLc: CG50907-02	17	18
MOL6	6A, 6B	MOL6: GMAC060288_A	19	20
MOL7	7A, 7B	MOL7: AF193808A	21	22
MOL8	8A, 8B	MOL8: SC84366578_A	23	24

MOLX Nucleic Acids and Polypeptides

One aspect of the invention pertains to isolated nucleic acid molecules that encode MOLX polypeptides or biologically active portions thereof. Also included in the invention are nucleic acid fragments sufficient for use as hybridization probes to identify MOLX-encoding nucleic acids (*e.g.*, MOLX mRNAs) and fragments for use as PCR primers for the amplification and/or mutation of MOLX nucleic acid molecules. As used herein, the term “nucleic acid molecule” is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule may be single-stranded or double-stranded, but preferably is comprised double-stranded DNA.

An MOLX nucleic acid can encode a mature MOLX polypeptide. As used herein, a “mature” form of a polypeptide or protein disclosed in the present invention is the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, by way of nonlimiting example, the full-length gene product, encoded by the corresponding gene. Alternatively, it may be defined as the polypeptide, precursor or proprotein encoded by an ORF described herein. The product “mature” form arises, again by way of nonlimiting example, as a result of one or more naturally occurring processing steps as they may take place within the cell, or host cell, in which the gene product arises. Examples of such processing steps leading to a “mature” form of a polypeptide or protein include the cleavage of the N-terminal methionine residue encoded

by the initiation codon of an ORF, or the proteolytic cleavage of a signal peptide or leader sequence. Thus a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining after removal of the N-terminal methionine. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues from residue M+1 to residue N remaining. Further as used herein, a "mature" form of a polypeptide or protein may arise from a step of post-translational modification other than a proteolytic cleavage event. Such additional processes include, by way of non-limiting example, glycosylation, myristoylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or a combination of any of them.

The term "probes", as utilized herein, refers to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as approximately, *e.g.*, 6,000 nt, depending upon the specific use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are generally obtained from a natural or recombinant source, are highly specific, and much slower to hybridize than shorter-length oligomer probes. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

The term "isolated" nucleic acid molecule, as utilized herein, is one, which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5'- and 3'-termini of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MOLX nucleic acid molecules can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell/tissue from which the nucleic acid is derived (*e.g.*, brain, heart, liver, spleen, etc.). Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23, or a complement of this aforementioned nucleotide sequence, can be isolated using standard

molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 as a hybridization probe, MOLX molecules can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook, *et al.*, (eds.), MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to MOLX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue.

Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment of the invention, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23, or a complement thereof. Oligonucleotides may be chemically synthesized and may also be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23, or a portion of this nucleotide sequence (*e.g.*, a fragment that can be used as a probe or primer or a fragment encoding a biologically-active portion of an MOLX polypeptide). A nucleic acid molecule that is complementary to the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 is one that is sufficiently complementary to the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23, thereby forming a stable duplex.

As used herein, the term “complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, van der Waals, hydrophobic interactions, and the like. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type. Homologs are nucleic acid sequences or amino acid sequences of a particular gene that are derived from different species.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, or 95% identity (with a preferred identity of 80-95%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below.

A “homologous nucleic acid sequence” or “homologous amino acid sequence,” or variations thereof, refer to sequences characterized by a homology at the nucleotide level or

amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of MOLX polypeptides. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA.

Alternatively, isoforms can be encoded by different genes. In the invention, homologous nucleotide sequences include nucleotide sequences encoding for an MOLX polypeptide of species other than humans, including, but not limited to: vertebrates, and thus can include, *e.g.*, frog, mouse, rat, rabbit, dog, cat, cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the exact nucleotide sequence encoding human MOLX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23, as well as a polypeptide possessing MOLX biological activity. Various biological activities of the MOLX proteins are described below.

An MOLX polypeptide is encoded by the open reading frame ("ORF") of an MOLX nucleic acid. An ORF corresponds to a nucleotide sequence that could potentially be translated into a polypeptide. A stretch of nucleic acids comprising an ORF is uninterrupted by a stop codon. An ORF that represents the coding sequence for a full protein begins with an ATG "start" codon and terminates with one of the three "stop" codons, namely, TAA, TAG, or TGA. For the purposes of this invention, an ORF may be any part of a coding sequence, with or without a start codon, a stop codon, or both. For an ORF to be considered as a good candidate for coding for a *bona fide* cellular protein, a minimum size requirement is often set, *e.g.*, a stretch of DNA that would encode a protein of 50 amino acids or more.

The nucleotide sequences determined from the cloning of the human MOLX genes allows for the generation of probes and primers designed for use in identifying and/or cloning MOLX homologues in other cell types, *e.g.* from other tissues, as well as MOLX homologues from other vertebrates. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 consecutive sense strand nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23; or an anti-sense strand nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23; or of a naturally occurring mutant of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23.

Probes based on the human MOLX nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissues which mis-express an MOLX protein, such as by measuring a level of an MOLX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting MOLX mRNA levels or determining whether a genomic MOLX gene has been mutated or deleted.

"A polypeptide having a biologically-active portion of an MOLX polypeptide" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically-active portion of MOLX" can be prepared by isolating a portion SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 that encodes a polypeptide having an MOLX biological activity (the biological activities of the MOLX proteins are described below), expressing the encoded portion of MOLX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of MOLX.

MOLX Nucleic Acid and Polypeptide Variants

The invention further encompasses nucleic acid molecules that differ from the nucleotide sequences shown SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 due to degeneracy of the genetic code and thus encode the same MOLX proteins as that encoded by the nucleotide sequences shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24.

In addition to the human MOLX nucleotide sequences shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of the MOLX polypeptides may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the MOLX genes may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame (ORF) encoding an MOLX protein, preferably a vertebrate MOLX protein. Such natural allelic variations can typically result in

1-5% variance in the nucleotide sequence of the MOLX genes. Any and all such nucleotide variations and resulting amino acid polymorphisms in the MOLX polypeptides, which are the result of natural allelic variation and that do not alter the functional activity of the MOLX polypeptides, are intended to be within the scope of the invention.

5 Moreover, nucleic acid molecules encoding MOLX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the MOLX cDNAs of the invention can be isolated based on their homology to the human MOLX
10 nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

 Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11,
15 13, 15, 17, 19, 21, and 23. In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500, 750, 1000, 1500, or 2000 or more nucleotides in length. In yet another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each
20 other typically remain hybridized to each other.

 Homologs (*i.e.*, nucleic acids encoding MOLX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

25 As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5 °C lower than the
30 thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in

which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at

pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and
5 oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y.

(1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%,

10 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions are hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C, followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated
15 nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequences of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

20 In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml
25 denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well-known within the art. See, *e.g.*, Ausubel, *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990; GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

30 In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequences of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02%

PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). See, *e.g.*,
 5 Ausubel, *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981. *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative Mutations

10 In addition to naturally-occurring allelic variants of MOLX sequences that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequences of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 thereby leading to changes in the amino acid sequences of the encoded MOLX proteins, without altering the functional ability of said MOLX proteins. For example,
 15 nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequences of the MOLX proteins without altering their biological activity, whereas an
 20 "essential" amino acid residue is required for such biological activity. For example, amino acid residues that are conserved among the MOLX proteins of the invention are predicted to be particularly non-amenable to alteration. Amino acids for which conservative substitutions can be made are well-known within the art.

Another aspect of the invention pertains to nucleic acid molecules encoding MOLX proteins that contain changes in amino acid residues that are not essential for activity. Such
 25 MOLX proteins differ in amino acid sequence from SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24 yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 45% homologous to the amino acid sequences of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24. Preferably, the protein encoded by the
 30 nucleic acid molecule is at least about 60% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24; more preferably at least about 70% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24; still more preferably at least about 80% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24; even more preferably at least about 90% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24; and most

preferably at least about 95% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24.

An isolated nucleic acid molecule encoding an MOLX protein homologous to the protein of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24 can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24 by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted, non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined within the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted non-essential amino acid residue in the MOLX protein is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MOLX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for MOLX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23, the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

The relatedness of amino acid families may also be determined based on side chain interactions. Substituted amino acids may be fully conserved "strong" residues or fully conserved "weak" residues. The "strong" group of conserved amino acid residues may be any one of the following groups: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW, wherein the single letter amino acid codes are grouped by those amino acids that may be substituted for each other. Likewise, the "weak" group of conserved residues may be any one of the following: CSA, ATV, SAG, STNK, STPA, SGND, SNDEQK, NDEQHK, NEQHRK, VLIM, HFY, wherein the letters within each group represent the single letter amino acid code.

In one embodiment, a mutant MOLX protein can be assayed for (i) the ability to form protein:protein interactions with other MOLX proteins, other cell-surface proteins, or biologically-active portions thereof, (ii) complex formation between a mutant MOLX protein and an MOLX ligand; or (iii) the ability of a mutant MOLX protein to bind to an intracellular target protein or biologically-active portion thereof; (*e.g.* avidin proteins).

In yet another embodiment, a mutant MOLX protein can be assayed for the ability to regulate a specific biological function (*e.g.*, regulation of insulin release).

Antisense Nucleic Acids

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein (*e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence). In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire MOLX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of an MOLX protein of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, or antisense nucleic acids complementary to an MOLX nucleic acid sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23, are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MOLX protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding the MOLX protein. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding the MOLX protein disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MOLX mRNA, but more preferably is an oligonucleotide that is

antisense to only a portion of the coding or noncoding region of MOLX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MOLX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention
 5 can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally-occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids (*e.g.*,
 10 phosphorothioate derivatives and acridine substituted nucleotides can be used).

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine,
 15 inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil,
 20 queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the
 25 inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MOLX protein to thereby inhibit expression of the protein (*e.g.*,
 30 by inhibiting transcription and/or translation). The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively,

antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface (e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens). The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient nucleic acid molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other. See, e.g., Gaultier, *et al.*, 1987. *Nucl. Acids Res.* **15**: 6625-6641. The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (see, e.g., Inoue, *et al.* 1987. *Nucl. Acids Res.* **15**: 6131-6148) or a chimeric RNA-DNA analogue (see, e.g., Inoue, *et al.*, 1987. *FEBS Lett.* **215**: 327-330).

Ribozymes and PNA Moieties

Nucleic acid modifications include, by way of non-limiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In one embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes as described in Haselhoff and Gerlach 1988. *Nature* **334**: 585-591) can be used to catalytically cleave MOLX mRNA transcripts to thereby inhibit translation of MOLX mRNA. A ribozyme having specificity for an MOLX-encoding nucleic acid can be designed based upon the nucleotide sequence of an MOLX cDNA disclosed herein (i.e., SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MOLX-encoding mRNA. See, e.g., U.S. Patent 4,987,071 to Cech, *et al.* and U.S. Patent 5,116,742 to Cech, *et al.* MOLX mRNA can also be

used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, MOLX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the MOLX nucleic acid (e.g., the MOLX promoter and/or enhancers) to form triple helical structures that prevent transcription of the MOLX gene in target cells. See, e.g., Helene, 1991. *Anticancer Drug Des.* 6: 569-84; Helene, *et al.* 1992. *Ann. N.Y. Acad. Sci.* 660: 27-36; Maher, 1992. *Bioassays* 14: 807-15.

In various embodiments, the MOLX nucleic acids can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids. See, e.g., Hyrup, *et al.*, 1996. *Bioorg Med Chem* 4: 5-23. As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics (e.g., DNA mimics) in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup, *et al.*, 1996. *supra*; Perry-O'Keefe, *et al.*, 1996. *Proc. Natl. Acad. Sci. USA* 93: 14670-14675.

PNAs of MOLX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of MOLX can also be used, for example, in the analysis of single base pair mutations in a gene (e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S₁ nucleases (see, Hyrup, *et al.*, 1996. *supra*); or as probes or primers for DNA sequence and hybridization (see, Hyrup, *et al.*, 1996, *supra*; Perry-O'Keefe, *et al.*, 1996. *supra*).

In another embodiment, PNAs of MOLX can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of MOLX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes (e.g., RNase H and DNA polymerases) to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking,

number of bonds between the nucleobases, and orientation (*see*, Hyrup, *et al.*, 1996. *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup, *et al.*, 1996. *supra* and Finn, *et al.*, 1996. *Nucl Acids Res* 24: 3357-3363. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA. *See, e.g.*, Mag, *et al.*, 1989. *Nucl Acid Res* 17: 5973-5988. PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment. *See, e.g.*, Finn, *et al.*, 1996. *supra*. Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. *See, e.g.*, Petersen, *et al.*, 1975. *Bioorg. Med. Chem. Lett.* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (*see, e.g.*, Letsinger, *et al.*, 1989. *Proc. Natl. Acad. Sci. U.S.A.* 86: 6553-6556; Lemaitre, *et al.*, 1987. *Proc. Natl. Acad. Sci.* 84: 648-652; PCT Publication No. WO88/09810) or the blood-brain barrier (*see, e.g.*, PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (*see, e.g.*, Krol, *et al.*, 1988. *BioTechniques* 6:958-976) or intercalating agents (*see, e.g.*, Zon, 1988. *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, and the like.

MOLX Polypeptides

A polypeptide according to the invention includes a polypeptide including the amino acid sequence of MOLX polypeptides whose sequences are provided in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residues shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24 while still encoding a protein that maintains its MOLX activities and physiological functions, or a functional fragment thereof.

In general, an MOLX variant that preserves MOLX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed

by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

One aspect of the invention pertains to isolated MOLX proteins, and biologically-active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided
5 are polypeptide fragments suitable for use as immunogens to raise anti-MOLX antibodies. In one embodiment, native MOLX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, MOLX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, an MOLX protein or polypeptide can be synthesized chemically
10 using standard peptide synthesis techniques.

An "isolated" or "purified" polypeptide or protein or biologically-active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the MOLX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free
15 of cellular material" includes preparations of MOLX proteins in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly-produced. In one embodiment, the language "substantially free of cellular material" includes preparations of MOLX proteins having less than about 30% (by dry weight) of non-MOLX proteins (also referred to herein as a "contaminating protein"), more preferably less than about 20% of
20 non-MOLX proteins, still more preferably less than about 10% of non-MOLX proteins, and most preferably less than about 5% of non-MOLX proteins. When the MOLX protein or biologically-active portion thereof is recombinantly-produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of
25 the MOLX protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of MOLX proteins in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations
30 of MOLX proteins having less than about 30% (by dry weight) of chemical precursors or non-MOLX chemicals, more preferably less than about 20% chemical precursors or non-MOLX chemicals, still more preferably less than about 10% chemical precursors or non-MOLX chemicals, and most preferably less than about 5% chemical precursors or non-MOLX chemicals.

Biologically-active portions of MOLX proteins include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequences of the MOLX proteins (*e.g.*, the amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24) that include fewer amino acids than the full-length MOLX proteins, and exhibit at least one activity of an MOLX protein. Typically, biologically-active portions comprise a domain or motif with at least one activity of the MOLX protein. A biologically-active portion of an MOLX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acid residues in length.

Moreover, other biologically-active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native MOLX protein.

In an embodiment, the MOLX protein has an amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24. In other embodiments, the MOLX protein is substantially homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, and retains the functional activity of the protein of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail, below. Accordingly, in another embodiment, the MOLX protein is a protein that comprises an amino acid sequence at least about 45% homologous to the amino acid sequence SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, and retains the functional activity of the MOLX proteins of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24.

Determining Homology Between Two or More Sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known

in the art, such as GAP software provided in the GCG program package. *See*, Needleman and Wunsch, 1970. *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above
5 exhibits a degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23.

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of
10 comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*,
15 the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a
20 reference sequence over a comparison region.

Chimeric and Fusion Proteins

The invention also provides MOLX chimeric or fusion proteins. As used herein, an MOLX "chimeric protein" or "fusion protein" comprises an MOLX polypeptide operatively-
25 linked to a non-MOLX polypeptide. An "MOLX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an MOLX protein (SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24), whereas a "non-MOLX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the MOLX protein, *e.g.*, a protein that is different from the MOLX protein and that is derived
30 from the same or a different organism. Within an MOLX fusion protein the MOLX polypeptide can correspond to all or a portion of an MOLX protein. In one embodiment, an MOLX fusion protein comprises at least one biologically-active portion of an MOLX protein. In another embodiment, an MOLX fusion protein comprises at least two biologically-active portions of an MOLX protein. In yet another embodiment, an MOLX fusion protein

comprises at least three biologically-active portions of an MOLX protein. Within the fusion protein, the term "operatively-linked" is intended to indicate that the MOLX polypeptide and the non-MOLX polypeptide are fused in-frame with one another. The non-MOLX polypeptide can be fused to the N-terminus or C-terminus of the MOLX polypeptide.

5 In one embodiment, the fusion protein is a GST-MOLX fusion protein in which the MOLX sequences are fused to the C-terminus of the GST (glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant MOLX polypeptides.

10 In another embodiment, the fusion protein is an MOLX protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of MOLX can be increased through use of a heterologous signal sequence.

In yet another embodiment, the fusion protein is an MOLX-immunoglobulin fusion protein in which the MOLX sequences are fused to sequences derived from a member of the immunoglobulin protein family. The MOLX-immunoglobulin fusion proteins of the invention
15 can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between an MOLX ligand and an MOLX protein on the surface of a cell, to thereby suppress MOLX-mediated signal transduction *in vivo*. The MOLX-immunoglobulin fusion proteins can be used to affect the bioavailability of an MOLX cognate ligand.
20 Inhibition of the MOLX ligand/MOLX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the MOLX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-MOLX antibodies in a subject, to purify MOLX ligands, and in screening assays to identify molecules that inhibit the interaction of
25 MOLX with an MOLX ligand.

An MOLX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction
30 enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two

consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (*see, e.g., Ausubel, et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992*). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g., a GST polypeptide*). An MOLX-encoding
5 nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MOLX protein.

MOLX Agonists and Antagonists

The invention also pertains to variants of the MOLX proteins that function as either
10 MOLX agonists (*i.e., mimetics*) or as MOLX antagonists. Variants of the MOLX protein can be generated by mutagenesis (*e.g., discrete point mutation or truncation of the MOLX protein*). An agonist of the MOLX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the MOLX protein. An antagonist of the MOLX protein can inhibit one or more of the activities of the naturally occurring form of
15 the MOLX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the MOLX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to
20 treatment with the naturally occurring form of the MOLX proteins.

Variants of the MOLX proteins that function as either MOLX agonists (*i.e., mimetics*) or as MOLX antagonists can be identified by screening combinatorial libraries of mutants (*e.g., truncation mutants*) of the MOLX proteins for MOLX protein agonist or antagonist activity. In one embodiment, a variegated library of MOLX variants is generated by
25 combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MOLX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MOLX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g., for phage display*) containing the set of
30 MOLX sequences therein. There are a variety of methods which can be used to produce libraries of potential MOLX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the

desired set of potential MOLX sequences. Methods for synthesizing degenerate oligonucleotides are well-known within the art. *See, e.g., Narang, 1983. Tetrahedron* 39: 3; Itakura, *et al.*, 1984. *Annu. Rev. Biochem.* 53: 323; Itakura, *et al.*, 1984. *Science* 198: 1056; Ike, *et al.*, 1983. *Nucl. Acids Res.* 11: 477.

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Polypeptide Libraries

In addition, libraries of fragments of the MOLX protein coding sequences can be used to generate a variegated population of MOLX fragments for screening and subsequent selection of variants of an MOLX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MOLX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double-stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S_1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, expression libraries can be derived which encodes N-terminal and internal fragments of various sizes of the MOLX proteins.

Various techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MOLX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MOLX variants. *See, e.g., Arkin and Yourvan, 1992. Proc. Natl. Acad. Sci. USA* 89: 7811-7815; Delgrave, *et al.*, 1993. *Protein Engineering* 6:327-331.

Anti-MOLX Antibodies

The invention encompasses antibodies and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any of the MOLX polypeptides of said invention.

An isolated MOLX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind to MOLX polypeptides using standard techniques for polyclonal and monoclonal antibody preparation. The full-length MOLX proteins can be used or, alternatively, the invention provides antigenic peptide fragments of MOLX proteins for use as immunogens. The antigenic MOLX peptides comprises at least 4 amino acid residues of the amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24 and encompasses an epitope of MOLX such that an antibody raised against the peptide forms a specific immune complex with MOLX. Preferably, the antigenic peptide comprises at least 6, 8, 10, 15, 20, or 30 amino acid residues. Longer antigenic peptides are sometimes preferable over shorter antigenic peptides, depending on use and according to methods well known to someone skilled in the art.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of MOLX that is located on the surface of the protein (*e.g.*, a hydrophilic region). As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation (*see, e.g.*, Hopp and Woods, 1981. *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle, 1982. *J. Mol. Biol.* 157: 105-142, each incorporated herein by reference in their entirety).

As disclosed herein, MOLX protein sequences of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, or derivatives, fragments, analogs or homologs thereof, may be utilized as immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically-active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically-binds (immunoreacts with) an antigen, such as MOLX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab)_2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human MOLX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to an MOLX protein sequence of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, or a derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic

preparation can contain, for example, recombinantly-expressed MOLX protein or a chemically-synthesized MOLX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against MOLX can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of MOLX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular MOLX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular MOLX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see, e.g., Kohler & Milstein, 1975. *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see, e.g., Kozbor, *et al.*, 1983. *Immunol. Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see, e.g., Cole, *et al.*, 1985. In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the invention and may be produced by using human hybridomas (see, e.g., Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see, e.g., Cole, *et al.*, 1985. In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations is incorporated herein by reference in their entirety.

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an MOLX protein (see, e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see, e.g., Huse, *et al.*, 1989. *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for an MOLX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See, e.g., U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to an MOLX protein may be produced by techniques known in the

art including, but not limited to: (i) an $F_{(ab)2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab)2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent; and (iv) F_v fragments.

5 Additionally, recombinant anti-MOLX antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in International Application
10 No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Patent No. 4,816,567; U.S. Pat. No. 5,225,539; European Patent Application No. 125,023; Better, *et al.*, 1988. *Science* 240: 1041-1043; Liu, *et al.*, 1987. *Proc. Natl. Acad. Sci. USA* 84: 3439-3443; Liu, *et al.*, 1987. *J. Immunol.* 139: 3521-3526; Sun,
15 *et al.*, 1987. *Proc. Natl. Acad. Sci. USA* 84: 214-218; Nishimura, *et al.*, 1987. *Cancer Res.* 47: 999-1005; Wood, *et al.*, 1985. *Nature* 314 :446-449; Shaw, *et al.*, 1988. *J. Natl. Cancer Inst.* 80: 1553-1559; Morrison(1985) *Science* 229:1202-1207; Oi, *et al.* (1986) *BioTechniques* 4:214; Jones, *et al.*, 1986. *Nature* 321: 552-525; Verhoevan, *et al.*, 1988. *Science* 239: 1534; and Beidler, *et al.*, 1988. *J. Immunol.* 141: 4053-4060. Each of the above citations are
20 incorporated herein by reference in their entirety.

 In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of an MOLX protein is
25 facilitated by generation of hybridomas that bind to the fragment of an MOLX protein possessing such a domain. Thus, antibodies that are specific for a desired domain within an MOLX protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

 Anti-MOLX antibodies may be used in methods known within the art relating to the
30 localization and/or quantitation of an MOLX protein (*e.g.*, for use in measuring levels of the MOLX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for MOLX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody

derived binding domain, are utilized as pharmacologically-active compounds (hereinafter "Therapeutics").

An anti-MOLX antibody (*e.g.*, monoclonal antibody) can be used to isolate an MOLX polypeptide by standard techniques, such as affinity chromatography or immunoprecipitation.

5 An anti-MOLX antibody can facilitate the purification of natural MOLX polypeptide from cells and of recombinantly-produced MOLX polypeptide expressed in host cells. Moreover, an anti-MOLX antibody can be used to detect MOLX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the MOLX protein. Anti-MOLX antibodies can be used diagnostically to monitor protein levels in tissue
10 as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish
15 peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include
20 luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

MOLX Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors,
25 containing a nucleic acid encoding an MOLX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA
30 segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome.

Moreover, certain vectors are capable of directing the expression of genes to which they are operatively-linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the
5 plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that
10 the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively-linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably-linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory
15 *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell).

The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN
20 ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be
25 transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, MOLX proteins, mutant forms of MOLX proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of
30 MOLX proteins in prokaryotic or eukaryotic cells. For example, MOLX proteins can be expressed in bacterial cells such as *Escherichia coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San

Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *Escherichia coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (i) to increase expression of recombinant protein; (ii) to increase the solubility of the recombinant protein; and (iii) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988. *Gene* 67: 31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, e.g., Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (see, e.g., Wada, *et al.*, 1992. *Nucl. Acids Res.* 20: 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MOLX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *Saccharomyces cerevisiae* include pYepSec1 (Baldari, *et al.*, 1987. *EMBO J.* 6: 229-234), pMFa (Kurjan and Herskowitz, 1982. *Cell* 30: 933-943), pJRY88 (Schultz *et al.*, 1987. *Gene* 54: 113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (InVitrogen Corp, San Diego, Calif.).

Alternatively, MOLX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, SF9 cells) include the pAc series (Smith, *et al.*, 1983. *Mol. Cell. Biol.* 3: 2156-2165) and the pVL series (Lucklow and Summers, 1989. *Virology* 170: 31-39).

5 In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987. *Nature* 329: 840) and pMT2PC (Kaufman, *et al.*, 1987. *EMBO J.* 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are
10 derived from polyoma, adenovirus 2, cytomegalovirus, and simian virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see, *e.g.*, Chapters 16 and 17 of Sambrook, *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of
15 directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert, *et al.*, 1987. *Genes Dev.* 1: 268-277), lymphoid-specific promoters (Calame and Eaton, 1988. *Adv. Immunol.* 43: 235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. *EMBO J.* 8: 729-733) and immunoglobulins (Banerji, *et al.*, 1983. *Cell* 33: 729-740; Queen and Baltimore, 1983. *Cell* 33: 741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle, 1989. *Proc. Natl. Acad. Sci. USA* 86: 5473-5477),
20 pancreas-specific promoters (Edlund, *et al.*, 1985. *Science* 230: 912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss, 1990. *Science* 249: 374-379) and the α -fetoprotein promoter (Campes and Tilghman, 1989. *Genes Dev.* 3: 537-546).

The invention further provides a recombinant expression vector comprising a DNA
30 molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively-linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to MOLX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA

molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes *see, e.g.,* Weintraub, *et al.*, "Antisense RNA as a molecular tool for genetic analysis," *Reviews-Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, MOLX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.,* DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.,* resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a

selectable marker can be introduced into a host cell on the same vector as that encoding MOLX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

5 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) MOLX protein. Accordingly, the invention further provides methods for producing MOLX protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding MOLX protein has been introduced) in a suitable
10 medium such that MOLX protein is produced. In another embodiment, the method further comprises isolating MOLX protein from the medium or the host cell.

Transgenic MOLX Animals

 The host cells of the invention can also be used to produce non-human transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or
15 an embryonic stem cell into which MOLX protein-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous MOLX sequences have been introduced into their genome or homologous recombinant animals in which endogenous MOLX sequences have been altered. Such animals are useful for studying the function and/or activity of MOLX protein and for identifying and/or
20 evaluating modulators of MOLX protein activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell
25 from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous MOLX gene has been altered by homologous recombination between the endogenous gene
30 and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

 A transgenic animal of the invention can be created by introducing MOLX-encoding nucleic acid into the male pronuclei of a fertilized oocyte (*e.g.*, by microinjection, retroviral

infection) and allowing the oocyte to develop in a pseudopregnant female foster animal. The human MOLX cDNA sequences of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 can be introduced as a transgene into the genome of a non-human animal. Alternatively, a non-human homologue of the human MOLX gene, such as a mouse MOLX gene, can be isolated based on hybridization to the human MOLX cDNA (described further *supra*) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably-linked to the MOLX transgene to direct expression of MOLX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan, 1986. In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the MOLX transgene in its genome and/or expression of MOLX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene-encoding MOLX protein can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of an MOLX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MOLX gene. The MOLX gene can be a human gene (*e.g.*, the cDNA of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23), but more preferably, is a non-human homologue of a human MOLX gene. For example, a mouse homologue of human MOLX gene of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 can be used to construct a homologous recombination vector suitable for altering an endogenous MOLX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous MOLX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MOLX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous MOLX protein). In the homologous recombination vector, the altered portion

of the MOLX gene is flanked at its 5'- and 3'-termini by additional nucleic acid of the MOLX gene to allow for homologous recombination to occur between the exogenous MOLX gene carried by the vector and an endogenous MOLX gene in an embryonic stem cell. The additional flanking MOLX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5'- and 3'-termini) are included in the vector. *See, e.g., Thomas, et al., 1987. Cell 51: 503* for a description of homologous recombination vectors. The vector is then introduced into an embryonic stem cell line (*e.g., by electroporation*) and cells in which the introduced MOLX gene has homologously-recombined with the endogenous MOLX gene are selected. *See, e.g., Li, et al., 1992. Cell 69: 915.*

The selected cells are then injected into a blastocyst of an animal (*e.g., a mouse*) to form aggregation chimeras. *See, e.g., Bradley, 1987. In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152.* A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously-recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously-recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, 1991. *Curr. Opin. Biotechnol. 2: 823-829*; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, *See, e.g., Lakso, et al., 1992. Proc. Natl. Acad. Sci. USA 89: 6232-6236.* Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae*. *See, O'Gorman, et al., 1991. Science 251:1351-1355.* If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, *e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.*

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut, *et al., 1997. Nature 385: 810-813.* In brief, a cell (*e.g., a somatic cell*) from the transgenic animal can be isolated and induced to exit the

growth cycle and enter G₀ phase. The quiescent cell can then be fused, *e.g.*, through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of this female foster animal will be a clone of the animal from which the cell (*e.g.*, the somatic cell) is isolated.

Pharmaceutical Compositions

The MOLX nucleic acid molecules, MOLX proteins, and anti-MOLX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (*i.e.*, topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be

adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous
5 solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under
10 the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by
15 the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the
20 composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (e.g., an MOLX protein or anti-MOLX antibody) in the required amount in an appropriate solvent
25 with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of
30 the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form

of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (*see, e.g.*, U.S. Patent No. 5,328,470) or by stereotactic injection (*see, e.g.*, Chen, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Screening and Detection Methods

The isolated nucleic acid molecules of the invention can be used to express MOLX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect MOLX mRNA (*e.g.*, in a biological sample) or a genetic lesion in an MOLX gene, and to modulate MOLX activity, as described further, below. In addition, the MOLX proteins can be used to screen drugs or compounds that modulate the MOLX protein activity or expression as well as to treat disorders characterized by insufficient or excessive production of MOLX protein or production of MOLX protein forms that have decreased or aberrant activity compared to MOLX wild-type protein (*e.g.*; diabetes (regulates insulin release); obesity (binds and transport lipids); metabolic disturbances associated with obesity, the metabolic syndrome X as well as anorexia and wasting disorders associated with chronic diseases and various cancers, and infectious disease (possesses anti-microbial activity) and the various dyslipidemias. In addition, the anti-MOLX antibodies of the invention can be used to detect

and isolate MOLX proteins and modulate MOLX activity. In yet a further aspect, the invention can be used in methods to influence appetite, absorption of nutrients and the disposition of metabolic substrates in both a positive and negative fashion.

5 The invention further pertains to novel agents identified by the screening assays described herein and uses thereof for treatments as described, *supra*.

Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, 10 peptidomimetics, small molecules or other drugs) that bind to MOLX proteins or have a stimulatory or inhibitory effect on, *e.g.*, MOLX protein expression or MOLX protein activity. The invention also includes compounds identified in the screening assays described herein.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of the membrane-bound form of an MOLX 15 protein or polypeptide or biologically-active portion thereof. The test compounds of the invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity 20 chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds. *See, e.g.*, Lam, 1997. *Anticancer Drug Design* 12: 145.

A "small molecule" as used herein, is meant to refer to a composition that has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small 25 molecules can be, *e.g.*, nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened with any of the assays of the invention.

Examples of methods for the synthesis of molecular libraries can be found in the art, 30 for example in: DeWitt, *et al.*, 1993. *Proc. Natl. Acad. Sci. U.S.A.* 90: 6909; Erb, *et al.*, 1994. *Proc. Natl. Acad. Sci. U.S.A.* 91: 11422; Zuckermann, *et al.*, 1994. *J. Med. Chem.* 37: 2678; Cho, *et al.*, 1993. *Science* 261: 1303; Carrell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2059; Carell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2061; and Gallop, *et al.*, 1994. *J. Med. Chem.* 37: 1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten, 1992. *Biotechniques* 13: 412-421), or on beads (Lam, 1991. *Nature* 354: 82-84), on chips (Fodor, 1993. *Nature* 364: 555-556), bacteria (Ladner, U.S. Patent No. 5,223,409), spores (Ladner, U.S. Patent 5,233,409), plasmids (Cull, *et al.*, 1992. *Proc. Natl. Acad. Sci. USA* 89: 1865-1869) or on phage (Scott and Smith, 1990. *Science* 249: 386-390; Devlin, 1990. *Science* 249: 404-406; Cwirla, *et al.*, 1990. *Proc. Natl. Acad. Sci. U.S.A.* 87: 6378-6382; Felici, 1991. *J. Mol. Biol.* 222: 301-310; Ladner, U.S. Patent No. 5,233,409.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of MOLX protein, or a biologically-active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to an MOLX protein determined. The cell, for example, can be of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the MOLX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the MOLX protein or biologically-active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically-labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of MOLX protein, or a biologically-active portion thereof, on the cell surface with a known compound which binds MOLX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an MOLX protein, wherein determining the ability of the test compound to interact with an MOLX protein comprises determining the ability of the test compound to preferentially bind to MOLX protein or a biologically-active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of MOLX protein, or a biologically-active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the MOLX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of MOLX or a biologically-active portion thereof can be accomplished, for example, by determining the ability of the MOLX protein to bind to or interact with an MOLX

target molecule. As used herein, a "target molecule" is a molecule with which an MOLX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses an MOLX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule associated with the internal surface of a cell membrane or a cytoplasmic molecule. An MOLX target molecule can be a non-MOLX molecule or an MOLX protein or polypeptide of the invention. In one embodiment, an MOLX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.* a signal generated by binding of a compound to a membrane-bound MOLX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with MOLX.

Determining the ability of the MOLX protein to bind to or interact with an MOLX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the MOLX protein to bind to or interact with an MOLX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+} , diacylglycerol, IP_3 , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising an MOLX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the invention is a cell-free assay comprising contacting an MOLX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to bind to the MOLX protein or biologically-active portion thereof. Binding of the test compound to the MOLX protein can be determined either directly or indirectly as described above. In one such embodiment, the assay comprises contacting the MOLX protein or biologically-active portion thereof with a known compound which binds MOLX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an MOLX protein, wherein determining the ability of the test compound to interact with an MOLX protein comprises determining the ability of the test compound to preferentially bind to MOLX or biologically-active portion thereof as compared to the known compound.

In still another embodiment, an assay is a cell-free assay comprising contacting MOLX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.* stimulate or inhibit) the activity of the MOLX protein or biologically-active portion thereof. Determining the ability of the test compound to
5 modulate the activity of MOLX can be accomplished, for example, by determining the ability of the MOLX protein to bind to an MOLX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of MOLX protein can be accomplished by
10 determining the ability of the MOLX protein further modulate an MOLX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as described, *supra*.

In yet another embodiment, the cell-free assay comprises contacting the MOLX protein or biologically-active portion thereof with a known compound which binds MOLX protein to form an assay mixture, contacting the assay mixture with a test compound, and determining
5 the ability of the test compound to interact with an MOLX protein, wherein determining the ability of the test compound to interact with an MOLX protein comprises determining the ability of the MOLX protein to preferentially bind to or modulate the activity of an MOLX target molecule.

The cell-free assays of the invention are amenable to use of both the soluble form or
10 the membrane-bound form of MOLX protein. In the case of cell-free assays comprising the membrane-bound form of MOLX protein, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of MOLX protein is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide,
15 decanoyl-N-methylglucamide, Triton[®] X-100, Triton[®] X-114, Thesit[®], Isotridecypoly(ethylene glycol ether)_n, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl) dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the invention, it may be
10 desirable to immobilize either MOLX protein or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to MOLX protein, or interaction of MOLX protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such

vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, GST-MOLX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or
5 glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or MOLX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex
10 determined either directly or indirectly, for example, as described, *supra*. Alternatively, the complexes can be dissociated from the matrix, and the level of MOLX protein binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either the MOLX protein or its target
5 molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated MOLX protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well-known within the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with MOLX protein or target
10 molecules, but which do not interfere with binding of the MOLX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or MOLX protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the MOLX protein or target molecule, as well as enzyme-linked
15 assays that rely on detecting an enzymatic activity associated with the MOLX protein or target molecule.

In another embodiment, modulators of MOLX protein expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of MOLX mRNA or protein in the cell is determined. The level of expression of MOLX mRNA or
20 protein in the presence of the candidate compound is compared to the level of expression of MOLX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of MOLX mRNA or protein expression based upon this comparison. For example, when expression of MOLX mRNA or protein is greater (*i.e.*, statistically significantly greater) in the presence of the candidate compound than in its

absence, the candidate compound is identified as a stimulator of MOLX mRNA or protein expression. Alternatively, when expression of MOLX mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of MOLX mRNA or protein expression. The level of
5 MOLX mRNA or protein expression in the cells can be determined by methods described herein for detecting MOLX mRNA or protein.

In yet another aspect of the invention, the MOLX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (*see, e.g.*, U.S. Patent No. 5,283,317; Zervos, *et al.*, 1993. *Cell* 72: 223-232; Madura, *et al.*, 1993. *J. Biol. Chem.* 268: 12046-12054;
10 Bartel, *et al.*, 1993. *Biotechniques* 14: 920-924; Iwabuchi, *et al.*, 1993. *Oncogene* 8: 1693-1696; and Brent WO 94/10300), to identify other proteins that bind to or interact with MOLX ("MOLX-binding proteins" or "MOLX-bp") and modulate MOLX activity. Such MOLX-binding proteins are also likely to be involved in the propagation of signals by the MOLX proteins as, for example, upstream or downstream elements of the MOLX pathway.

15 The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for MOLX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an
20 unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming an MOLX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional
25 regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with MOLX.

The invention further pertains to novel agents identified by the aforementioned screening assays and uses thereof for treatments as described herein.

30 Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. By way of example, and not of limitation, these sequences can be used to: (i) map their respective

genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Some of these applications are described in the subsections, below.

5

Chromosome Mapping

Once the sequence (or a portion of the sequence) of a gene has been isolated, this sequence can be used to map the location of the gene on a chromosome. This process is called chromosome mapping. Accordingly, portions or fragments of the MOLX sequences, SEQ ID
10 NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23, or fragments or derivatives thereof, can be used to map the location of the MOLX genes, respectively, on a chromosome. The mapping of the MOLX sequences to chromosomes is an important first step in correlating these sequences with genes associated with disease.

Briefly, MOLX genes can be mapped to chromosomes by preparing PCR primers
15 (preferably 15-25 bp in length) from the MOLX sequences. Computer analysis of the MOLX sequences can be used to rapidly select primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers can then be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the MOLX sequences will yield an
20 amplified fragment.

Somatic cell hybrids are prepared by fusing somatic cells from different mammals (e.g., human and mouse cells). As hybrids of human and mouse cells grow and divide, they gradually lose human chromosomes in random order, but retain the mouse chromosomes. By using media in which mouse cells cannot grow, because they lack a particular enzyme, but in
25 which human cells can, the one human chromosome that contains the gene encoding the needed enzyme will be retained. By using various media, panels of hybrid cell lines can be established. Each cell line in a panel contains either a single human chromosome or a small number of human chromosomes, and a full set of mouse chromosomes, allowing easy mapping of individual genes to specific human chromosomes. See, e.g., D'Eustachio, *et al.*,
30 1983. *Science* 220: 919-924. Somatic cell hybrids containing only fragments of human chromosomes can also be produced by using human chromosomes with translocations and deletions.

PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular sequence to a particular chromosome. Three or more sequences can be assigned per day using

a single thermal cycler. Using the MOLX sequences to design oligonucleotide primers, sub-localization can be achieved with panels of fragments from specific chromosomes.

Fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase chromosomal spread can further be used to provide a precise chromosomal location in one step. Chromosome spreads can be made using cells whose division has been blocked in metaphase by a chemical like colcemid that disrupts the mitotic spindle. The chromosomes can be treated briefly with trypsin, and then stained with Giemsa. A pattern of light and dark bands develops on each chromosome, so that the chromosomes can be identified individually. The FISH technique can be used with a DNA sequence as short as 500 or 600 bases.

However, clones larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. Preferably 1,000 bases, and more preferably 2,000 bases, will suffice to get good results at a reasonable amount of time. For a review of this technique, *see*, Verma, *et al.*, HUMAN CHROMOSOMES: A MANUAL OF BASIC TECHNIQUES (Pergamon Press, New York 1988).

Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found, *e.g.*, in McKusick, MENDELIAN INHERITANCE IN MAN, available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and disease, mapped to the same chromosomal region, can then be identified through linkage analysis (co-inheritance of physically adjacent genes), described in, *e.g.*, Egeland, *et al.*, 1987. *Nature*, 325: 783-787.

Moreover, differences in the DNA sequences between individuals affected and unaffected with a disease associated with the MOLX gene, can be determined. If a mutation is observed in some or all of the affected individuals but not in any unaffected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and unaffected individuals generally involves first looking for structural alterations in the chromosomes, such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence. Ultimately, complete

sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

Tissue Typing

5 The MOLX sequences of the invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Patent No. 5,272,057).

10 Furthermore, the sequences of the invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the MOLX sequences described herein can be used to prepare two PCR primers from the 5'- and 3'-termini of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

15 Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the invention can be used to obtain such identification sequences from individuals and from tissue. The MOLX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to
20 some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

25 Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a
30 noncoding amplified sequence of 100 bases. If predicted coding sequences, such as those in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the invention relates to diagnostic assays for determining MOLX protein and/or nucleic acid expression as well as MOLX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant MOLX expression or activity. The disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with MOLX protein, nucleic acid expression or activity. For example, mutations in an MOLX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with MOLX protein, nucleic acid expression, or biological activity.

Another aspect of the invention provides methods for determining MOLX protein, nucleic acid expression or activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of MOLX in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

An exemplary method for detecting the presence or absence of MOLX in a biological sample involves obtaining a biological sample from a test subject and contacting the biological

sample with a compound or an agent capable of detecting MOLX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes MOLX protein such that the presence of MOLX is detected in the biological sample. An agent for detecting MOLX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to MOLX mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length MOLX nucleic acid, such as the nucleic acid of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to MOLX mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays of the invention are described herein.

An agent for detecting MOLX protein is an antibody capable of binding to MOLX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect MOLX mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of MOLX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of MOLX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of MOLX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of MOLX protein include introducing into a subject a labeled anti-MOLX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting MOLX protein, mRNA, or genomic DNA, such that the presence of MOLX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of MOLX protein, mRNA or genomic DNA in the control sample with the presence of MOLX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of MOLX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting MOLX protein or mRNA in a biological sample; means for determining the amount of MOLX in the sample; and means for comparing the amount of MOLX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect MOLX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant MOLX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with MOLX protein, nucleic acid expression or activity. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the invention provides a method for identifying a disease or disorder associated with aberrant MOLX expression or activity in which a test sample is obtained from a subject and MOLX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of MOLX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant MOLX expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant MOLX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder. Thus, the invention provides methods for determining whether a subject can be effectively

5 treated with an agent for a disorder associated with aberrant MOLX expression or activity in which a test sample is obtained and MOLX protein or nucleic acid is detected (*e.g.*, wherein the presence of MOLX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant MOLX expression or activity).

10 The methods of the invention can also be used to detect genetic lesions in an MOLX gene, thereby determining if a subject with the lesioned gene is at risk for a disorder characterized by aberrant cell proliferation and/or differentiation. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding an MOLX-protein, or the misexpression of the MOLX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of: (i) a deletion of one or more nucleotides from an MOLX gene; (ii) an addition of one or more nucleotides to an MOLX gene; (iii) a substitution of one or more nucleotides of an MOLX gene, (iv) a chromosomal rearrangement of an MOLX gene; (v) an alteration in the level of a messenger RNA transcript of an MOLX gene, (vi) aberrant modification of an MOLX gene, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild-type splicing pattern of a messenger RNA transcript of an MOLX gene, (viii) a non-wild-type level of an MOLX protein, (ix) allelic loss of an MOLX gene, and (x) inappropriate post-translational modification of an MOLX protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in an MOLX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

25 In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (*see, e.g.*, U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (*see, e.g.*, Landegran, *et al.*, 1988. *Science* 241: 1077-1080; and Nakazawa, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 360-364), the latter of which can be particularly useful for detecting point mutations in the MOLX-gene (*see*, Abravaya, *et al.*, 1995. *Nucl. Acids Res.* 23: 675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to an MOLX gene under conditions such that hybridization and amplification of the MOLX gene (if present)

occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

5 Alternative amplification methods include: self sustained sequence replication (*see*, Guatelli, *et al.*, 1990. *Proc. Natl. Acad. Sci. USA* 87: 1874-1878), transcriptional amplification system (*see*, Kwok, *et al.*, 1989. *Proc. Natl. Acad. Sci. USA* 86: 1173-1177); Q β Replicase (*see*, Lizardi, *et al.*, 1988. *BioTechnology* 6: 1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to
10 those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in an MOLX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction
15 endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (*see, e.g.*, U.S. Patent No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

20 In other embodiments, genetic mutations in MOLX can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high-density arrays containing hundreds or thousands of oligonucleotides probes. *See, e.g.*, Cronin, *et al.*, 1996. *Human Mutation* 7: 244-255; Kozal, *et al.*, 1996. *Nat. Med.* 2: 753-759. For example, genetic mutations in MOLX can be identified in two dimensional arrays containing light-generated
25 DNA probes as described in Cronin, *et al.*, *supra*. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This is followed by a second hybridization array that allows the characterization of specific mutations by using smaller,
30 specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the MOLX gene and detect mutations by comparing the

sequence of the sample MOLX with the corresponding wild-type (control) sequence.

Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert, 1977. *Proc. Natl. Acad. Sci. USA* 74: 560 or Sanger, 1977. *Proc. Natl. Acad. Sci. USA* 74: 5463. It is also contemplated that any of a variety of automated sequencing procedures

5 can be utilized when performing the diagnostic assays (*see, e.g., Naeve, et al., 1995.*

Biotechniques 19: 448), including sequencing by mass spectrometry (*see, e.g., PCT International Publication No. WO 94/16101; Cohen, et al., 1996. Adv. Chromatography* 36: 127-162; and Griffin, *et al., 1993. Appl. Biochem. Biotechnol.* 38: 147-159).

Other methods for detecting mutations in the MOLX gene include methods in which
10 protection from cleavage agents is used to detect mismatched bases in RNA/RNA or
RNA/DNA heteroduplexes. *See, e.g., Myers, et al., 1985. Science* 230: 1242. In general, the
art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by
hybridizing (labeled) RNA or DNA containing the wild-type MOLX sequence with potentially
mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are
15 treated with an agent that cleaves single-stranded regions of the duplex such as which will
exist due to basepair mismatches between the control and sample strands. For instance,
RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S₁
nuclease to enzymatically digesting the mismatched regions. In other embodiments, either
DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide
20 and with piperidine in order to digest mismatched regions. After digestion of the mismatched
regions, the resulting material is then separated by size on denaturing polyacrylamide gels to
determine the site of mutation. *See, e.g., Cotton, et al., 1988. Proc. Natl. Acad. Sci. USA* 85:
4397; Saleeba, *et al., 1992. Methods Enzymol.* 217: 286-295. In an embodiment, the control
DNA or RNA can be labeled for detection.

25 In still another embodiment, the mismatch cleavage reaction employs one or more
proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA
mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in
MOLX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli*
cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T
30 at G/T mismatches. *See, e.g., Hsu, et al., 1994. Carcinogenesis* 15: 1657-1662. According to
an exemplary embodiment, a probe based on an MOLX sequence, *e.g., a wild-type MOLX*
sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is
treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be
detected from electrophoresis protocols or the like. *See, e.g., U.S. Patent No. 5,459,039.*

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in MOLX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids. *See, e.g., Orita, et al., 1989. Proc. Natl. Acad. Sci. USA: 86: 2766; Cotton,*
5 *1993. Mutat. Res. 285: 125-144; Hayashi, 1992. Genet. Anal. Tech. Appl. 9: 73-79.*

Single-stranded DNA fragments of sample and control MOLX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled
10 probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. *See, e.g., Keen, et al., 1991. Trends Genet. 7: 5.*

15 In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). *See, e.g., Myers, et al., 1985. Nature 313: 495.* When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich
20 DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. *See, e.g., Rosenbaum and Reissner, 1987. Biophys. Chem. 265: 12753.*

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer
25 extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. *See, e.g., Saiki, et al., 1986. Nature 324: 163; Saiki, et al., 1989. Proc. Natl. Acad. Sci. USA 86: 6230.* Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the
30 oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the

molecule (so that amplification depends on differential hybridization; *see, e.g., Gibbs, et al., 1989. Nucl. Acids Res.* 17: 2437-2448) or at the extreme 3'-terminus of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (*see, e.g., Prossner, 1993. Tibtech.* 11: 238). In addition it may be desirable to introduce a novel
5 restriction site in the region of the mutation to create cleavage-based detection. *See, e.g., Gasparini, et al., 1992. Mol. Cell Probes* 6: 1. It is anticipated that in certain embodiments amplification may also be performed using *Taq* ligase for amplification. *See, e.g., Barany, 1991. Proc. Natl. Acad. Sci. USA* 88: 189. In such cases, ligation will occur only if there is a perfect match at the 3'-terminus of the 5' sequence, making it possible to detect the presence of
10 a known mutation at a specific site by looking for the presence or absence of amplification.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.,* in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving an MOLX
15 gene.

Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which MOLX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.
20

Pharmacogenomics

Agents, or modulators that have a stimulatory or inhibitory effect on MOLX activity (*e.g.,* MOLX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (The
25 disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.) In conjunction with such
30 treatment, the pharmacogenomics (*i.e.,* the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the

selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of MOLX protein, expression of MOLX nucleic acid, or mutation content of MOLX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996. *Clin. Exp. Pharmacol. Physiol.*, 23: 983-985; Linder, 1997. *Clin. Chem.*, 43: 254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of MOLX protein, expression of MOLX nucleic acid, or mutation content of MOLX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an MOLX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring of Effects During Clinical Trials

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of MOLX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase MOLX gene expression, protein levels, or upregulate MOLX activity, can be monitored in clinical trials of subjects exhibiting decreased MOLX gene expression, protein levels, or downregulated MOLX activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease MOLX gene expression, protein levels, or downregulate MOLX activity, can be monitored in clinical trials of subjects exhibiting increased MOLX gene expression, protein levels, or upregulated MOLX activity. In such clinical trials, the expression or activity of MOLX and, preferably, other genes that have been implicated in, for example, a cellular proliferation or immune disorder can be used as a "read out" or markers of the immune responsiveness of a particular cell.

By way of example, and not of limitation, genes, including MOLX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates MOLX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of MOLX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of MOLX or other genes. In this manner, the gene expression pattern can serve as a marker, indicative of the physiological

response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, peptidomimetic, nucleic acid, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of an MOLX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression or activity of the MOLX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the MOLX protein, mRNA, or genomic DNA in the pre-administration sample with the MOLX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of MOLX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of MOLX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant MOLX expression or activity. The disorders include cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate cancer, neoplasm; adenocarcinoma, lymphoma, uterus cancer, fertility, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial asthma, Crohn's disease; multiple sclerosis, treatment of Albright Hereditary Osteodystrophy, and other diseases, disorders and conditions of the like.

These methods of treatment will be discussed more fully, below.

Disease and Disorders

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with
5 Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to: (i) an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to an aforementioned peptide; (iii) nucleic acids encoding an aforementioned peptide; (iv) administration of antisense nucleic acid
10 and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to an aforementioned peptide) that are utilized to "knockout" endogenous function of an aforementioned peptide by homologous recombination (*see, e.g.*, Capecchi, 1989. *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or
15 antibodies specific to a peptide of the invention) that alter the interaction between an aforementioned peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with
20 Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for
25 RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of an aforementioned peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in*
30 *situ* hybridization, and the like).

Prophylactic Methods

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant MOLX expression or activity, by administering to the

subject an agent that modulates MOLX expression or at least one MOLX activity. Subjects at risk for a disease that is caused or contributed to by aberrant MOLX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the MOLX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending upon the type of MOLX aberrancy, for example, an MOLX agonist or MOLX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein. The prophylactic methods of the invention are further discussed in the following subsections.

Therapeutic Methods

Another aspect of the invention pertains to methods of modulating MOLX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of MOLX protein activity associated with the cell. An agent that modulates MOLX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of an MOLX protein, a peptide, an MOLX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more MOLX protein activity. Examples of such stimulatory agents include active MOLX protein and a nucleic acid molecule encoding MOLX that has been introduced into the cell. In another embodiment, the agent inhibits one or more MOLX protein activity. Examples of such inhibitory agents include antisense MOLX nucleic acid molecules and anti-MOLX antibodies. These modulatory methods can be performed *in vitro* (e.g., by culturing the cell with the agent) or, alternatively, *in vivo* (e.g., by administering the agent to a subject). As such, the invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of an MOLX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (e.g., an agent identified by a screening assay described herein), or combination of agents that modulates (e.g., up-regulates or down-regulates) MOLX expression or activity. In another embodiment, the method involves administering an MOLX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant MOLX expression or activity.

Stimulation of MOLX activity is desirable in situations in which MOLX is abnormally downregulated and/or in which increased MOLX activity is likely to have a beneficial effect.

One example of such a situation is where a subject has a disorder characterized by aberrant cell proliferation and/or differentiation (*e.g.*, cancer or immune associated disorders). Another example of such a situation is where the subject has a gestational disease (*e.g.*, preclampsia).

Determination of the Biological Effect of the Therapeutic

5 In various embodiments of the invention, suitable *in vitro* or *in vivo* assays are performed to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

 In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts
10 the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

15 Prophylactic and Therapeutic Uses of the Compositions of the Invention

 The MOLX nucleic acids and proteins of the invention are useful in potential prophylactic and therapeutic applications implicated in a variety of disorders including, but not limited to: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder,
20 immune disorders, hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.

 As an example, a cDNA encoding the MOLX protein of the invention may be useful in gene therapy, and the protein may be useful when administered to a subject in need thereof.
25 By way of non-limiting example, the compositions of the invention will have efficacy for treatment of patients suffering from: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, hematopoietic disorders, and the various dyslipidemias.

30 Both the novel nucleic acid encoding the MOLX protein, and the MOLX protein of the invention, or fragments thereof, may also be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. A further use could be as an anti-bacterial molecule (*i.e.*, some peptides have been found to possess anti-bacterial

properties). These materials are further useful in the generation of antibodies which immunospecifically-bind to the novel substances of the invention for use in therapeutic or diagnostic methods.

Examples

5 Example 1. Quantitative expression analysis of clones in various cells and tissues

The quantitative expression of various clones was assessed using microtiter plates containing RNA samples from a variety of normal and pathology-derived cells, cell lines and tissues using real time quantitative PCR (RTQ PCR; TAQMAN®). RTQ PCR was performed on a Perkin-Elmer Biosystems ABI PRISM® 7700 Sequence Detection System. Various
0 collections of samples are assembled on the plates, and referred to as Panel 1 (containing cells and cell lines from normal and cancer sources), Panel 2 (containing samples derived from tissues, in particular from surgical samples, from normal and cancer sources), Panel 3 (containing samples derived from a wide variety of cancer sources), Panel 4 (containing cells and cell lines from normal cells and cells related to inflammatory conditions) and Panel
5 CNSD.01 (containing samples from normal and diseased brains).

First, the RNA samples were normalized to constitutively expressed genes such as β -actin and GAPDH. RNA (~50 ng total or ~1 ng polyA+) was converted to cDNA using the TAQMAN® Reverse Transcription Reagents Kit (PE Biosystems, Foster City, CA; Catalog No. N808-0234) and random hexamers according to the manufacturer's protocol. Reactions
10 were performed in 20 ul and incubated for 30 min. at 48°C. cDNA (5 ul) was then transferred to a separate plate for the TAQMAN® reaction using β -actin and GAPDH TAQMAN® Assay Reagents (PE Biosystems; Catalog Nos. 4310881E and 4310884E, respectively) and TAQMAN® universal PCR Master Mix (PE Biosystems; Catalog No. 4304447) according to the manufacturer's protocol. Reactions were performed in 25 ul using the following
15 parameters: 2 min. at 50°C; 10 min. at 95°C; 15 sec. at 95°C/1 min. at 60°C (40 cycles). Results were recorded as CT values (cycle at which a given sample crosses a threshold level of fluorescence) using a log scale, with the difference in RNA concentration between a given sample and the sample with the lowest CT value being represented as 2 to the power of delta CT. The percent relative expression is then obtained by taking the reciprocal of this RNA
20 difference and multiplying by 100. The average CT values obtained for β -actin and GAPDH were used to normalize RNA samples. The RNA sample generating the highest CT value required no further diluting, while all other samples were diluted relative to this sample according to their β -actin /GAPDH average CT values.

Normalized RNA (5 ul) was converted to cDNA and analyzed via TAQMAN® using One Step RT-PCR Master Mix Reagents (PE Biosystems; Catalog No. 4309169) and gene-specific primers according to the manufacturer's instructions. Probes and primers were designed for each assay according to Perkin Elmer Biosystem's *Primer Express* Software package (version I for Apple Computer's Macintosh Power PC) or a similar algorithm using the target sequence as input. Default settings were used for reaction conditions and the following parameters were set before selecting primers: primer concentration = 250 nM, primer melting temperature (T_m) range = 58°-60° C, primer optimal T_m = 59° C, maximum primer difference = 2° C, probe does not have 5' G, probe T_m must be 10° C greater than primer T_m , amplicon size 75 bp to 100 bp. The probes and primers selected (see below) were synthesized by Synthegen (Houston, TX, USA). Probes were double purified by HPLC to remove uncoupled dye and evaluated by mass spectroscopy to verify coupling of reporter and quencher dyes to the 5' and 3' ends of the probe, respectively. Their final concentrations were: forward and reverse primers, 900 nM each, and probe, 200nM.

PCR conditions:

Normalized RNA from each tissue and each cell line was spotted in each well of a 96 well PCR plate (Perkin Elmer Biosystems). PCR cocktails including two probes (a probe specific for the target clone and another gene-specific probe multiplexed with the target probe) were set up using 1X TaqMan™ PCR Master Mix for the PE Biosystems 7700, with 5 mM MgCl₂, dNTPs (dA, G, C, U at 1:1:1:2 ratios), 0.25 U/ml AmpliTaq Gold™ (PE Biosystems), and 0.4 U/μl RNase inhibitor, and 0.25 U/μl reverse transcriptase. Reverse transcription was performed at 48° C for 30 minutes followed by amplification/PCR cycles as follows: 95° C 10 min, then 40 cycles of 95° C for 15 seconds, 60° C for 1 minute.

In the results for Panel 1, the following abbreviations are used:

ca. = carcinoma,

* = established from metastasis,

met = metastasis,

s cell var= small cell variant,

non-s = non-sm =non-small,

squam = squamous,

pl. eff = pl effusion = pleural effusion,

glio = glioma,

astro = astrocytoma, and

neuro = neuroblastoma.

Panel 2

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The plates for Panel 2 generally include 2 control wells and 94 test samples composed of RNA or cDNA isolated from human tissue procured by surgeons working in close cooperation with the National Cancer Institute's Cooperative Human Tissue Network (CHTN) or the National Disease Research Initiative (NDRI). The tissues are derived from human malignancies and in cases where indicated many malignant tissues have "matched margins" obtained from noncancerous tissue just adjacent to the tumor. These are termed normal adjacent tissues and are denoted "NAT" in the results below. The tumor tissue and the "matched margins" are evaluated by two independent pathologists (the surgical pathologists and again by a pathologists at NDRI or CHTN). This analysis provides a gross histopathological assessment of tumor differentiation grade. Moreover, most samples include the original surgical pathology report that provides information regarding the clinical stage of the patient. These matched margins are taken from the tissue surrounding (i.e. immediately proximal) to the zone of surgery (designated "NAT", for normal adjacent tissue, in Table RR). In addition, RNA and cDNA samples were obtained from various human tissues derived from autopsies performed on elderly people or sudden death victims (accidents, etc.). These tissues were ascertained to be free of disease and were purchased from various commercial sources such as Clontech (Palo Alto, CA), Research Genetics, and Invitrogen.

25

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

Panel 3D

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The plates of Panel 3D are comprised of 94 cDNA samples and two control samples. Specifically, 92 of these samples are derived from cultured human cancer cell lines, 2 samples of human primary cerebellar tissue and 2 controls. The human cell lines are generally

obtained from ATCC (American Type Culture Collection, Manassas, VA), National Cancer Institute or the German tumor cell bank and fall into the following tissue groups: Squamous cell carcinoma of the tongue, breast cancer, prostate cancer, melanoma, epidermoid carcinoma, sarcomas, bladder carcinomas, pancreatic cancers, kidney cancers, leukemias/lymphomas, ovarian/uterine/cervical, gastric, colon, lung and CNS cancer cell lines. In addition, there are two independent samples of cerebellum. These cells are all cultured under standard recommended conditions and RNA extracted using the standard procedures. The cell lines in panel 3D and 1.3D are of the most common cell lines used in the scientific literature.

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

Panel 4

Panel 4 includes samples on a 96 well plate (2 control wells, 94 test samples) composed of RNA (Panel 4r) or cDNA (Panel 4d) isolated from various human cell lines or tissues related to inflammatory conditions. Total RNA from control normal tissues such as colon and lung (Stratagene, La Jolla, CA) and thymus and kidney (Clontech) were employed. Total RNA from liver tissue from cirrhosis patients and kidney from lupus patients was obtained from BioChain (Biochain Institute, Inc., Hayward, CA). Intestinal tissue for RNA preparation from patients diagnosed as having Crohn's disease and ulcerative colitis was obtained from the National Disease Research Interchange (NDRI) (Philadelphia, PA).

Astrocytes, lung fibroblasts, dermal fibroblasts, coronary artery smooth muscle cells, small airway epithelium, bronchial epithelium, microvascular dermal endothelial cells, microvascular lung endothelial cells, human pulmonary aortic endothelial cells, human umbilical vein endothelial cells were all purchased from Clonetics (Walkersville, MD) and grown in the media supplied for these cell types by Clonetics. These primary cell types were activated with various cytokines or combinations of cytokines for 6 and/or 12-14 hours, as indicated. The following cytokines were used; IL-1 beta at approximately 1-5 ng/ml, TNF alpha at approximately 5-10 ng/ml, IFN gamma at approximately 20-50 ng/ml, IL-4 at

approximately 5-10 ng/ml, IL-9 at approximately 5-10 ng/ml, IL-13 at approximately 5-10 ng/ml. Endothelial cells were sometimes starved for various times by culture in the basal media from Clonetics with 0.1% serum.

Mononuclear cells were prepared from blood of employees at CuraGen Corporation, using Ficoll. LAK cells were prepared from these cells by culture in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco/Life Technologies, Rockville, MD), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and Interleukin 2 for 4-6 days. Cells were then either activated with 10-20 ng/ml PMA and 1-2 μ g/ml ionomycin, IL-12 at 5-10 ng/ml, IFN gamma at 20-50 ng/ml and IL-18 at 5-10 ng/ml for 6 hours. In some cases, mononuclear cells were cultured for 4-5 days in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) with PHA (phytohemagglutinin) or PWM (pokeweed mitogen) at approximately 5 μ g/ml. Samples were taken at 24, 48 and 72 hours for RNA preparation. MLR (mixed lymphocyte reaction) samples were obtained by taking blood from two donors, isolating the mononuclear cells using Ficoll and mixing the isolated mononuclear cells 1:1 at a final concentration of approximately 2×10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol (5.5×10^{-5} M) (Gibco), and 10 mM Hepes (Gibco). The MLR was cultured and samples taken at various time points ranging from 1- 7 days for RNA preparation.

Monocytes were isolated from mononuclear cells using CD14 Miltenyi Beads, +ve VS selection columns and a Vario Magnet according to the manufacturer's instructions. Monocytes were differentiated into dendritic cells by culture in DMEM 5% fetal calf serum (FCS) (Hyclone, Logan, UT), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco), 50 ng/ml GMCSF and 5 ng/ml IL-4 for 5-7 days. Macrophages were prepared by culture of monocytes for 5-7 days in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and 10% AB Human Serum or MCSF at approximately 50 ng/ml. Monocytes, macrophages and dendritic cells were stimulated for 6 and 12-14 hours with lipopolysaccharide (LPS) at 100 ng/ml. Dendritic cells were also stimulated with anti-CD40 monoclonal antibody (Pharmingen) at 10 μ g/ml for 6 and 12-14 hours.

CD4 lymphocytes, CD8 lymphocytes and NK cells were also isolated from mononuclear cells using CD4, CD8 and CD56 Miltenyi beads, positive VS selection columns

and a Vario Magnet according to the manufacturer's instructions. CD45RA and CD45RO CD4 lymphocytes were isolated by depleting mononuclear cells of CD8, CD56, CD14 and CD19 cells using CD8, CD56, CD14 and CD19 Miltenyi beads and positive selection. Then CD45RO beads were used to isolate the CD45RO CD4 lymphocytes with the remaining cells being CD45RA CD4 lymphocytes. CD45RA CD4, CD45RO CD4 and CD8 lymphocytes were placed in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and plated at 10^6 cells/ml onto Falcon 6 well tissue culture plates that had been coated overnight with 0.5 μ g/ml anti-CD28 (Pharmingen) and 3 μ g/ml anti-CD3 (OKT3, ATCC) in PBS. After 6 and 24 hours, the cells were harvested for RNA preparation. To prepare chronically activated CD8 lymphocytes, we activated the isolated CD8 lymphocytes for 4 days on anti-CD28 and anti-CD3 coated plates and then harvested the cells and expanded them in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and IL-2. The expanded CD8 cells were then activated again with plate bound anti-CD3 and anti-CD28 for 4 days and expanded as before. RNA was isolated 6 and 24 hours after the second activation and after 4 days of the second expansion culture. The isolated NK cells were cultured in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and IL-2 for 4-6 days before RNA was prepared.

To obtain B cells, tonsils were procured from NDRI. The tonsil was cut up with sterile dissecting scissors and then passed through a sieve. Tonsil cells were then spun down and resuspended at 10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco). To activate the cells, we used PWM at 5 μ g/ml or anti-CD40 (Pharmingen) at approximately 10 μ g/ml and IL-4 at 5-10 ng/ml. Cells were harvested for RNA preparation at 24, 48 and 72 hours.

To prepare the primary and secondary Th1/Th2 and Tr1 cells, six-well Falcon plates were coated overnight with 10 μ g/ml anti-CD28 (Pharmingen) and 2 μ g/ml OKT3 (ATCC), and then washed twice with PBS. Umbilical cord blood CD4 lymphocytes (Poietic Systems, German Town, MD) were cultured at 10^5 - 10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and IL-2 (4 ng/ml). IL-12 (5 ng/ml) and anti-IL4 (1 μ g/ml) were used to direct to Th1, while IL-4 (5 ng/ml) and anti-IFN gamma (1 μ g/ml) were

used to direct to Th2 and IL-10 at 5 ng/ml was used to direct to Tr1. After 4-5 days, the activated Th1, Th2 and Tr1 lymphocytes were washed once in DMEM and expanded for 4-7 days in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco) and IL-2 (1 ng/ml). Following this, the activated Th1, Th2 and Tr1 lymphocytes were re-stimulated for 5 days with anti-CD28/OKT3 and cytokines as described above, but with the addition of anti-CD95L (1 μ g/ml) to prevent apoptosis. After 4-5 days, the Th1, Th2 and Tr1 lymphocytes were washed and then expanded again with IL-2 for 4-7 days. Activated Th1 and Th2 lymphocytes were maintained in this way for a maximum of three cycles. RNA was prepared from primary and secondary Th1, Th2 and Tr1 after 6 and 24 hours following the second and third activations with plate bound anti-CD3 and anti-CD28 mAbs and 4 days into the second and third expansion cultures in Interleukin 2.

The following leukocyte cells lines were obtained from the ATCC: Ramos, EOL-1, KU-812. EOL cells were further differentiated by culture in 0.1 mM dbcAMP at 5×10^5 cells/ml for 8 days, changing the media every 3 days and adjusting the cell concentration to 5×10^5 cells/ml. For the culture of these cells, we used DMEM or RPMI (as recommended by the ATCC), with the addition of 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10 mM Hepes (Gibco). RNA was either prepared from resting cells or cells activated with PMA at 10 ng/ml and ionomycin at 1 μ g/ml for 6 and 14 hours. Keratinocyte line CCD106 and an airway epithelial tumor line NCI-H292 were also obtained from the ATCC. Both were cultured in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10 mM Hepes (Gibco). CCD1106 cells were activated for 6 and 14 hours with approximately 5 ng/ml TNF alpha and 1 ng/ml IL-1 beta, while NCI-H292 cells were activated for 6 and 14 hours with the following cytokines: 5 ng/ml IL-4, 5 ng/ml IL-9, 5 ng/ml IL-13 and 25 ng/ml IFN gamma.

For these cell lines and blood cells, RNA was prepared by lysing approximately 10^7 cells/ml using Trizol (Gibco BRL). Briefly, 1/10 volume of bromochloropropane (Molecular Research Corporation) was added to the RNA sample, vortexed and after 10 minutes at room temperature, the tubes were spun at 14,000 rpm in a Sorvall SS34 rotor. The aqueous phase was removed and placed in a 15 ml Falcon Tube. An equal volume of isopropanol was added and left at -20 degrees C overnight. The precipitated RNA was spun down at 9,000 rpm for 15 min in a Sorvall SS34 rotor and washed in 70% ethanol. The pellet was redissolved in 300 μ l of RNase-free water and 35 μ l buffer (Promega) 5 μ l DTT, 7 μ l

RNAasin and 8 µl DNase were added. The tube was incubated at 37 degrees C for 30 minutes to remove contaminating genomic DNA, extracted once with phenol chloroform and re-precipitated with 1/10 volume of 3 M sodium acetate and 2 volumes of 100% ethanol. The RNA was spun down and placed in RNase free water. RNA was stored at -80 degrees C.

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Panel CNSD.01

The plates for Panel CNSD.01 include two control wells and 94 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard
10 Brain Tissue Resource Center. Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

Disease diagnoses are taken from patient records. The panel contains two brains from
5 each of the following diagnoses: Alzheimer's disease, Parkinson's disease, Huntington's disease, Progressive Supranuclear Palsy, Depression, and "Normal controls". Within each of these brains, the following regions are represented: cingulate gyrus, temporal pole, globus pallidus, substantia nigra, Brodman Area 4 (primary motor strip), Brodman Area 7 (parietal cortex), Brodman Area 9 (prefrontal cortex), and Brodman area 17 (occipital cortex). Not all
10 brain regions are represented in all cases; e.g., Huntington's disease is characterized in part by neurodegeneration in the globus pallidus, thus this region is impossible to obtain from confirmed Huntington's cases. Likewise Parkinson's disease is characterized by degeneration of the substantia nigra making this region more difficult to obtain. Normal control brains were examined for neuropathology and found to be free of any pathology consistent with
15 neurodegeneration.

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA
20 contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

In the labels employed to identify tissues in the CNS panel, the following abbreviations are used:

PSP = Progressive supranuclear palsy

Sub Nigra = Substantia nigra

Glob Palladus= Globus palladus

Temp Pole = Temporal pole

5 Cing Gyr = Cingulate gyrus

BA 4 = Brodman Area 4

10 A. MOL1a

Expression of gene SC29674552_EXT was assessed using the primer-probe sets Ag267 and Ag1308, described in Tables 10 and 11. Results of the RTQ-PCR runs are shown in Tables 12, 13, 14, 15, and 16

15 **Table 10. Probe Name Ag267**

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-TGCAGCGACCATCGTTCA-3'		18	50	65
Probe	TET-5'- CTGCTGTAACATTTCATCAATCTGGTCACTGCA-3'- TAMRA		32	76	66
Reverse	5'-GGGTACATGGGCGCCAT-3'		17	109	67

Table 11. Probe Name: Ag1308

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-GAGTGTGACATTCCAGGACACT-3'	59.1	22	139	68
Probe	FAM-5'-ATGGTGGCACCTGCCTCAACCTG-3'- TAMRA	71.6	23	167	69
Reverse	5'-GCACTGGCACTGGTAGGAA-3'	59.8	19	195	70

20 **Table 12. Panel 1**

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	1tm420t_ ag267		1tm420t_ ag267
Endothelial cells	4.4	Kidney (fetal)	19.8
Endothelial cells (treated)	5.3	Renal ca. 786-0	17.4

Pancreas	11.5	Renal ca. A498	20.6
Pancreatic ca. CAPAN 2	7.0	Renal ca. RXF 393	18.4
Adipose	40.3	Renal ca. ACHN	20.4
Adrenal gland	5.8	Renal ca. UO-31	20.3
Thyroid	11.5	Renal ca. TK-10	100.0
Salivary gland	7.5	Liver	7.3
Pituitary gland	4.9	Liver (fetal)	2.3
Brain (fetal)	1.2	Liver ca. (hepatoblast) HepG2	0.0
Brain (whole)	7.9	Lung	5.4
Brain (amygdala)	5.3	Lung (fetal)	4.2
Brain (cerebellum)	16.6	Lung ca. (small cell) LX-1	2.8
Brain (hippocampus)	1.8	Lung ca. (small cell) NCI-H69	5.5
Brain (substantia nigra)	2.0	Lung ca. (s.cell var.) SHP-77	3.2
Brain (thalamus)	1.6	Lung ca. (large cell) NCI-H460	6.7
Brain (hypothalamus)	0.9	Lung ca. (non-sm. cell) A549	6.5
Spinal cord	3.0	Lung ca. (non-s.cell) NCI-H23	9.0
CNS ca. (glio/astro) U87-MG	70.7	Lung ca (non-s.cell) HOP-62	14.4
CNS ca. (glio/astro) U-118-MG	21.6	Lung ca. (non-s.cl) NCI-H522	56.6
CNS ca. (astro) SW1783	20.7	Lung ca. (squam.) SW 900	28.1
CNS ca.* (neuro; met) SK-N-AS	0.0	Lung ca. (squam.) NCI-H596	2.9
CNS ca. (astro) SF-539	14.6	Mammary gland	35.1
CNS ca. (astro) SNB-75	15.8	Breast ca.* (pl. effusion) MCF-7	32.3
CNS ca. (glio) SNB-19	62.8	Breast ca.* (pl.ef) MDA-MB-231	19.6
CNS ca. (glio) U251	5.9	Breast ca.* (pl. effusion) T47D	19.1
CNS ca. (glio) SF-295	23.0	Breast ca. BT-549	11.0
Heart	5.7	Breast ca. MDA-N	7.9
Skeletal muscle	1.3	Ovary	44.4
Bone marrow	4.1	Ovarian ca. OVCAR-3	15.9
Thymus	32.3	Ovarian ca. OVCAR-4	44.4
Spleen	3.4	Ovarian ca. OVCAR-5	30.1
Lymph node	5.0	Ovarian ca. OVCAR-8	50.7
Colon (ascending)	16.8	Ovarian ca. IGROV-1	10.4
Stomach	11.1	Ovarian ca.* (ascites) SK-OV-3	11.9
Small intestine	2.6	Uterus	8.3
Colon ca. SW480	6.2	Placenta	21.0
Colon ca.* (SW480 met)SW620	0.9	Prostate	11.3
Colon ca. HT29	6.2	Prostate ca.* (bone met)PC-3	22.2
Colon ca. HCT-116	19.2	Testis	92.0
Colon ca. CaCo-2	15.0	Melanoma Hs688(A).T	13.5
Colon ca. HCT-15	20.2	Melanoma* (met) Hs688(B).T	20.3
Colon ca. HCC-2998	3.9	Melanoma UACC-62	8.5
Gastric ca.* (liver met) NCI-N87	22.8	Melanoma M14	15.2

Bladder	13.3	Melanoma LOX IMVI	54.7
Trachea	10.3	Melanoma* (met) SK-MEL-5	6.8
Kidney	6.4	Melanoma SK-MEL-28	38.4

Table 13. Panel 1.2

Tissue Name	Relative Expression(%) 1.2tm1287t_ ag267	Tissue Name	Relative Expression(%) 1.2tm1287t_ ag267
Endothelial cells	8.2	Renal ca. 786-0	16.8
Endothelial cells (treated)	15.0	Renal ca. A498	32.5
Pancreas	1.4	Renal ca. RXF 393	15.6
Pancreatic ca. CAPAN 2	2.9	Renal ca. ACHN	15.3
Adrenal Gland (new lot*)	14.7	Renal ca. UO-31	15.9
Thyroid	2.1	Renal ca. TK-10	53.2
Salivary gland	14.8	Liver	7.7
Pituitary gland	3.2	Liver (fetal)	3.8
Brain (fetal)	1.9	Liver ca. (hepatoblast) HepG2	0.0
Brain (whole)	7.1	Lung	6.0
Brain (amygdala)	7.7	Lung (fetal)	3.6
Brain (cerebellum)	5.0	Lung ca. (small cell) LX-1	2.0
Brain (hippocampus)	8.7	Lung ca. (small cell) NCI-H69	4.5
Brain (thalamus)	1.5	Lung ca. (s.cell var.) SHP-77	0.3
Cerebral Cortex	52.8	Lung ca. (large cell) NCI-H460	14.8
Spinal cord	6.4	Lung ca. (non-sm. cell) A549	8.3
CNS ca. (glio/astro) U87-MG	100.0	Lung ca. (non-s.cell) NCI-H23	13.4
CNS ca. (glio/astro) U-118-MG	37.1	Lung ca (non-s.cell) HOP-62	30.4
CNS ca. (astro) SW1783	14.2	Lung ca. (non-s.cl) NCI-H522	57.4
CNS ca.* (neuro; met) SK-N-AS	0.1	Lung ca. (squam.) SW 900	20.9
CNS ca. (astro) SF-539	11.9	Lung ca. (squam.) NCI-H596	2.7
CNS ca. (astro) SNB-75	9.6	Mammary gland	13.3
CNS ca. (glio) SNB-19	80.7	Breast ca.* (pl. effusion) MCF-7	31.9
CNS ca. (glio) U251	26.6	Breast ca.* (pl.ef) MDA-MB-231	23.7
CNS ca. (glio) SF-295	6.6	Breast ca.* (pl. effusion) T47D	12.2
Heart	21.0	Breast ca. BT-549	11.7
Skeletal Muscle (new lot*)	4.9	Breast ca. MDA-N	12.2
Bone marrow	2.2	Ovary	34.2
Thymus	2.1	Ovarian ca. OVCAR-3	35.8
Spleen	2.7	Ovarian ca. OVCAR-4	32.3
Lymph node	9.9	Ovarian ca. OVCAR-5	21.0
Colorectal	8.8	Ovarian ca. OVCAR-8	32.5
Stomach	8.7	Ovarian ca. IGROV-1	20.0

Small intestine	4.2	Ovarian ca.* (ascites) SK-OV-3	22.2
Colon ca. SW480	2.5	Uterus	5.2
Colon ca.* (SW480 met)SW620	0.5	Placenta	24.3
Colon ca. HT29	1.4	Prostate	9.2
Colon ca. HCT-116	13.4	Prostate ca.* (bone met)PC-3	30.6
Colon ca. CaCo-2	7.5	Testis	8.7
83219 CC Well to Mod Diff (ODO3866)	6.9	Melanoma Hs688(A).T	10.4
Colon ca. HCC-2998	14.7	Melanoma* (met) Hs688(B).T	15.8
Gastric ca.* (liver met) NCI-N87	38.2	Melanoma UACC-62	27.0
Bladder	37.1	Melanoma M14	13.1
Trachea	3.5	Melanoma LOX IMVI	8.4
Kidney	7.3	Melanoma* (met) SK-MEL-5	12.9
Kidney (fetal)	29.5	Adipose	27.5

Table 14. Panel 2D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	2Dtm2336t_ ag267		2Dtm2336t_ ag267
Normal Colon GENPAK 061003	23.7	Kidney NAT Clontech 8120608	7.7
83219 CC Well to Mod Diff (ODO3866)	6.1	Kidney Cancer Clontech 8120613	0.7
83220 CC NAT (ODO3866)	8.2	Kidney NAT Clontech 8120614	10.2
83221 CC Gr.2 rectosigmoid (ODO3868)	3.8	Kidney Cancer Clontech 9010320	24.0
83222 CC NAT (ODO3868)	3.5	Kidney NAT Clontech 9010321	24.3
83235 CC Mod Diff (ODO3920)	3.7	Normal Uterus GENPAK 061018	8.4
83236 CC NAT (ODO3920)	6.4	Uterus Cancer GENPAK 064011	15.5
83237 CC Gr.2 ascend colon (ODO3921)	7.5	Normal Thyroid Clontech A+ 6570-1	11.0
83238 CC NAT (ODO3921)	4.0	Thyroid Cancer GENPAK 064010	27.9
83241 CC from Partial Hepatectomy (ODO4309)	7.6	Thyroid Cancer INVITROGEN A302152	14.0
83242 Liver NAT (ODO4309)	7.5	Thyroid NAT INVITROGEN A302153	21.6
87472 Colon mets to lung (OD04451-01)	6.0	Normal Breast GENPAK 061019	33.7
87473 Lung NAT (OD04451- 02)	8.4	84877 Breast Cancer (OD04566)	11.9
Normal Prostate Clontech A+	7.7	85975 Breast Cancer	18.3

6546-1		(OD04590-01)	
84140 Prostate Cancer (OD04410)	22.1	85976 Breast Cancer Mets (OD04590-03)	37.1
84141 Prostate NAT (OD04410)	19.8	87070 Breast Cancer Metastasis (OD04655-05)	31.4
87073 Prostate Cancer (OD04720-01)	12.5	GENPAK Breast Cancer 064006	15.2
87074 Prostate NAT (OD04720-02)	27.5	Breast Cancer Res. Gen. 1024	30.8
Normal Lung GENPAK 061010	21.5	Breast Cancer Clontech 9100266	100.0
83239 Lung Met to Muscle (ODO4286)	10.2	Breast NAT Clontech 9100265	45.4
83240 Muscle NAT (ODO4286)	10.2	Breast Cancer INVITROGEN A209073	29.3
84136 Lung Malignant Cancer (OD03126)	16.0	Breast NAT INVITROGEN A2090734	26.1
84137 Lung NAT (OD03126)	15.9	Normal Liver GENPAK 061009	6.1
84871 Lung Cancer (OD04404)	8.0	Liver Cancer GENPAK 064003	11.7
84872 Lung NAT (OD04404)	19.2	Liver Cancer Research Genetics RNA 1025	6.4
84875 Lung Cancer (OD04565)	3.4	Liver Cancer Research Genetics RNA 1026	10.6
84876 Lung NAT (OD04565)	8.4	Paired Liver Cancer Tissue Research Genetics RNA 6004- T	14.7
85950 Lung Cancer (OD04237- 01)	27.4	Paired Liver Tissue Research Genetics RNA 6004-N	4.4
85970 Lung NAT (OD04237- 02)	15.8	Paired Liver Cancer Tissue Research Genetics RNA 6005- T	11.5
83255 Ocular Mel Met to Liver (ODO4310)	11.0	Paired Liver Tissue Research Genetics RNA 6005-N	5.4
83256 Liver NAT (ODO4310)	7.0	Normal Bladder GENPAK 061001	19.5
84139 Melanoma Mets to Lung (OD04321)	12.1	Bladder Cancer Research Genetics RNA 1023	9.3
84138 Lung NAT (OD04321)	23.5	Bladder Cancer INVITROGEN A302173	14.7
Normal Kidney GENPAK 061008	25.2	87071 Bladder Cancer (OD04718-01)	13.3
83786 Kidney Ca, Nuclear grade 2 (OD04338)	24.1	87072 Bladder Normal Adjacent (OD04718-03)	17.3
83787 Kidney NAT (OD04338)	7.7	Normal Ovary Res. Gen.	14.5
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	14.5	Ovarian Cancer GENPAK 064008	26.8
83789 Kidney NAT (OD04339)	9.2	87492 Ovary Cancer (OD04768-07)	15.5
83790 Kidney Ca, Clear cell type (OD04340)	19.9	87493 Ovary NAT (OD04768- 08)	9.9
83791 Kidney NAT (OD04340)	15.3	Normal Stomach GENPAK 061017	6.3

83792 Kidney Ca, Nuclear grade 3 (OD04348)	14.6	Gastric Cancer Clontech 9060358	3.7
83793 Kidney NAT (OD04348)	14.3	NAT Stomach Clontech 9060359	5.0
87474 Kidney Cancer (OD04622-01)	19.3	Gastric Cancer Clontech 9060395	11.8
87475 Kidney NAT (OD04622-03)	5.3	NAT Stomach Clontech 9060394	5.9
85973 Kidney Cancer (OD04450-01)	17.2	Gastric Cancer Clontech 9060397	14.5
85974 Kidney NAT (OD04450-03)	10.4	NAT Stomach Clontech 9060396	2.8
Kidney Cancer Clontech 8120607	17.9	Gastric Cancer GENPAK 064005	5.7

Table 15. Panel 2.2

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	2.2x4tm6515f_ag1308_b2		2.2x4tm6515f_ag1308_b2
Normal Colon GENPAK 061003	26.3	83793 Kidney NAT (OD04348)	83.7
97759 Colon cancer (OD06064)	20.5	98938 Kidney malignant cancer (OD06204B)	9.7
97760 Colon cancer NAT (OD06064)	6.5	98939 Kidney normal adjacent tissue (OD06204E)	15.3
97778 Colon cancer (OD06159)	2.6	85973 Kidney Cancer (OD04450-01)	55.1
97779 Colon cancer NAT (OD06159)	17.2	85974 Kidney NAT (OD04450-03)	23.4
98861 Colon cancer (OD06297-04)	2.7	Kidney Cancer Clontech 8120613	2.1
98862 Colon cancer NAT (OD06297-015)	25.9	Kidney NAT Clontech 8120614	12.5
83237 CC Gr.2 ascend colon (ODO3921)	9.2	Kidney Cancer Clontech 9010320	12.6
83238 CC NAT (ODO3921)	11.3	Kidney NAT Clontech 9010321	7.0
97766 Colon cancer metastasis (OD06104)	5.4	Kidney Cancer Clontech 8120607	19.0
97767 Lung NAT (OD06104)	4.6	Kidney NAT Clontech 8120608	6.5
87472 Colon mets to lung (OD04451-01)	22.6	Normal Uterus GENPAK 061018	31.5
87473 Lung NAT (OD04451-02)	18.3	Uterus Cancer GENPAK 064011	21.4
Normal Prostate Clontech A+ 6546-1 (8090438)	7.2	Normal Thyroid Clontech A+ 6570-1 (7080817)	1.2
84140 Prostate Cancer (OD04410)	11.0	Thyroid Cancer GENPAK 064010	16.7
84141 Prostate NAT (OD04410)	20.3	Thyroid Cancer INVITROGEN A302152	44.5

Normal Ovary Res. Gen.	29.1	Thyroid NAT INVITROGEN A302153	14.0
98863 Ovarian cancer (OD06283-03)	31.5	Normal Breast GENPAK 061019	39.9
98865 Ovarian cancer NAT/fallopian tube (OD06283-07)	19.3	84877 Breast Cancer (OD04566)	11.0
Ovarian Cancer GENPAK 064008	22.2	Breast Cancer Res. Gen. 1024	49.2
97773 Ovarian cancer (OD06145)	12.4	85975 Breast Cancer (OD04590-01)	50.8
97775 Ovarian cancer NAT (OD06145)	36.2	85976 Breast Cancer Mets (OD04590-03)	42.9
98853 Ovarian cancer (OD06455-03)	9.3	87070 Breast Cancer Metastasis (OD04655-05)	72.1
98854 Ovarian NAT (OD06455-07) Fallopian tube	7.6	GENPAK Breast Cancer 064006	29.0
Normal Lung GENPAK 061010	25.4	Breast Cancer Clontech 9100266	41.1
92337 Invasive poor diff. lung adeno (ODO4945-01)	10.9	Breast NAT Clontech 9100265	15.6
92338 Lung NAT (ODO4945-03)	20.2	Breast Cancer INVITROGEN A209073	13.5
84136 Lung Malignant Cancer (OD03126)	10.5	Breast NAT INVITROGEN A2090734	43.8
84137 Lung NAT (OD03126)	24.5	97763 Breast cancer (OD06083)	49.6
90372 Lung Cancer (OD05014A)	25.9	97764 Breast cancer node metastasis (OD06083)	44.3
90373 Lung NAT (OD05014B)	26.1	Normal Liver GENPAK 061009	38.6
97761 Lung cancer (OD06081)	8.3	Liver Cancer Research Genetics RNA 1026	13.2
97762 Lung cancer NAT (OD06081)	19.4	Liver Cancer Research Genetics RNA 1025	36.4
85950 Lung Cancer (OD04237-01)	13.3	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	23.8
85970 Lung NAT (OD04237-02)	41.6	Paired Liver Tissue Research Genetics RNA 6004-N	5.9
83255 Ocular Mel Met to Liver (ODO4310)	12.9	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	25.1
83256 Liver NAT (ODO4310)	11.5	Paired Liver Tissue Research Genetics RNA 6005-N	47.4
84139 Melanoma Mets to Lung (OD04321)	22.9	Liver Cancer GENPAK 064003	36.9
84138 Lung NAT (OD04321)	13.6	Normal Bladder GENPAK 061001	18.9
Normal Kidney GENPAK 061008	19.9	Bladder Cancer Research Genetics RNA 1023	9.6
83786 Kidney Ca, Nuclear grade 2 (OD04338)	59.8	Bladder Cancer INVITROGEN A302173	24.5

83787 Kidney NAT (OD04338)	23.8	Normal Stomach GENPAK 061017	43.1
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	100.0	Gastric Cancer Clontech 9060397	6.2
83789 Kidney NAT (OD04339)	7.3	NAT Stomach Clontech 9060396	7.3
83790 Kidney Ca, Clear cell type (OD04340)	15.0	Gastric Cancer Clontech 9060395	9.3
83791 Kidney NAT (OD04340)	22.5	NAT Stomach Clontech 9060394	13.3
83792 Kidney Ca, Nuclear grade 3 (OD04348)	14.3	Gastric Cancer GENPAK 064005	9.4

Table 16. Panel 4D

Tissue Name	Relative Expression(%)	Relative Expression(%)
	4Dtm1935t_ ag267	4Dtm1888f_ ag1308
93768 Secondary Th1 anti-CD28/anti-CD3	51.0	23.2
93769 Secondary Th2 anti-CD28/anti-CD3	43.5	24.1
93770 Secondary Tr1 anti-CD28/anti-CD3	42.6	23.8
93573 Secondary Th1 resting day 4-6 in IL-2	11.7	7.4
93572 Secondary Th2 resting day 4-6 in IL-2	21.9	12.4
93571 Secondary Tr1 resting day 4-6 in IL-2	12.1	8.0
93568 primary Th1 anti-CD28/anti-CD3	47.0	29.5
93569 primary Th2 anti-CD28/anti-CD3	28.1	22.8
93570 primary Tr1 anti-CD28/anti-CD3	45.1	37.9
93565 primary Th1 resting dy 4-6 in IL-2	51.8	49.3
93566 primary Th2 resting dy 4-6 in IL-2	23.0	27.9
93567 primary Tr1 resting dy 4-6 in IL-2	34.2	27.4
93351 CD45RA CD4 lymphocyte anti-CD28/anti-CD3	32.3	16.5
93352 CD45RO CD4 lymphocyte anti-CD28/anti-CD3	52.5	29.3
93251 CD8 Lymphocytes anti-CD28/anti-CD3	22.8	14.9
93353 chronic CD8 Lymphocytes 2ry resting dy 4-6 in IL-2	20.2	12.6
93574 chronic CD8 Lymphocytes 2ry activated CD3/CD28	22.1	14.2
93354 CD4 none	6.8	8.0
93252 Secondary Th1/Th2/Tr1 anti-CD95 CH11	31.0	23.0
93103 LAK cells resting	62.0	30.8
93788 LAK cells IL-2	47.3	27.4
93787 LAK cells IL-2+IL-12	41.5	23.3
93789 LAK cells IL-2+IFN gamma	36.1	27.4
93790 LAK cells IL-2+ IL-18	27.0	19.8
93104 LAK cells PMA/ionomycin and IL-18	38.2	21.2
93578 NK Cells IL-2 resting	17.0	14.7
93109 Mixed Lymphocyte Reaction Two Way MLR	30.8	27.7
93110 Mixed Lymphocyte Reaction Two Way MLR	19.6	12.2

93111_Mixed Lymphocyte Reaction_Two Way MLR	17.3	10.4
93112_Mononuclear Cells (PBMCs) resting	23.0	17.2
93113_Mononuclear Cells (PBMCs) PWM	91.4	56.6
93114_Mononuclear Cells (PBMCs) PHA-L	52.5	31.9
93249_Ramos (B cell) none	14.6	14.7
93250_Ramos (B cell) ionomycin	18.2	21.9
93349_B lymphocytes PWM	43.2	30.6
93350_B lymphocytes CD40L and IL-4	12.7	11.3
92665_EOL-1 (Eosinophil) dbcAMP differentiated	5.4	5.7
93248_EOL-1 (Eosinophil) dbcAMP/PMAionomycin	14.2	12.9
93356_Dendritic Cells none	28.5	16.2
93355_Dendritic Cells LPS 100 ng/ml	23.0	14.7
93775_Dendritic Cells anti-CD40	21.5	12.3
93774_Monocytes resting	81.8	58.2
93776_Monocytes LPS 50 ng/ml	100.0	100.0
93581_Macrophages resting	75.3	33.4
93582_Macrophages LPS 100 ng/ml	54.3	30.8
93098_HUVEC (Endothelial) none	12.7	6.3
93099_HUVEC (Endothelial) starved	18.3	12.7
93100_HUVEC (Endothelial) IL-1b	6.9	4.9
93779_HUVEC (Endothelial) IFN gamma	11.7	6.9
93102_HUVEC (Endothelial) TNF alpha + IFN gamma	12.9	6.4
93101_HUVEC (Endothelial) TNF alpha + IL4	20.7	10.7
93781_HUVEC (Endothelial) IL-11	4.8	2.8
93583_Lung Microvascular Endothelial Cells none	14.8	7.4
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	25.3	9.8
92662_Microvascular Dermal endothelium none	27.4	16.4
92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	40.3	17.8
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	37.6	24.1
93347_Small Airway Epithelium none	11.6	7.3
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	81.8	53.2
92668_Coronary Artery SMC resting	38.2	24.5
92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	32.3	24.0
93107_astrocytes resting	14.7	8.6
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	24.7	14.2
92666_KU-812 (Basophil) resting	12.4	9.9
92667_KU-812 (Basophil) PMA/ionomycin	46.7	29.3
93579_CCD1106 (Keratinocytes) none	13.7	8.9
93580_CCD1106 (Keratinocytes) TNFa and IFNg **	81.8	57.4
93791_Liver Cirrhosis	5.4	4.3
93792_Lupus Kidney	6.6	6.4
93577_NCI-H292	32.8	27.4

93358_NCI-H292_IL-4	41.8	34.9
93360_NCI-H292_IL-9	33.4	29.7
93359_NCI-H292_IL-13	27.0	21.9
93357_NCI-H292_IFN gamma	18.6	15.1
93777_HPAEC_-	7.5	4.6
93778_HPAEC_IL-1 beta/TNA alpha	26.6	14.5
93254_Normal Human Lung Fibroblast none	27.0	12.9
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	11.7	7.5
93257_Normal Human Lung Fibroblast_IL-4	31.9	15.9
93256_Normal Human Lung Fibroblast_IL-9	0.0	12.8
93255_Normal Human Lung Fibroblast_IL-13	38.7	26.6
93258_Normal Human Lung Fibroblast_IFN gamma	52.5	26.1
93106_Dermal Fibroblasts CCD1070_resting	57.0	34.9
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	87.1	60.7
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	46.7	37.4
93772_dermal fibroblast_IFN gamma	28.9	14.5
93771_dermal fibroblast_IL-4	51.0	27.7
93259_IBD Colitis 1**	4.9	4.8
93260_IBD Colitis 2	1.1	0.8
93261_IBD Crohns	1.0	1.0
735010_Colon_normal	12.4	6.7
735019_Lung_none	24.7	11.7
64028-1_Thymus_none	33.4	27.5
64030-1_Kidney_none	22.5	20.6

Panel 1 Summary: Ag267 Among the normal tissues on this panel, highest expression of the MOL1a gene is detected in testis (CT value = 25) and adipose. High expression in adipose might suggest that the MOL1a gene plays a role in the development of metabolic diseases, such as obesity or diabetes. In addition, expression of this gene is high in a renal cancer cell line (CT value = 25). Moderate expression of the MOL1a gene is also seen in most regions of normal brain. Strikingly, the MOL1a transcript appears at much higher levels in a number of CNS cancer cell lines. Therefore, inhibition of the MOL1a gene product using a monoclonal antibody and/or small molecule therapeutic may be useful for the treatment of some renal cell and CNS carcinomas.

Panel 1.2 Summary: Ag267 Expression of the MOL1a gene is highest in the cerebral cortex (CT value = 25) with more moderate expression detected in most other regions of normal brain, suggesting a role for this gene in neurological function. Consistent with the results seen in Panel 1, this gene is strikingly overexpressed in a number of CNS cancer cell lines (specifically glioma and astrocytoma). Moderate overexpression of the MOL1a gene is also detected in renal cell cancer and lung cancer cell lines relative to the normal controls. The

MOL1a gene product displays moderate similarity to the Notch protein that has been shown to be involved in cell signalling and has been implicated in oncogenesis. Therefore, the MOL1a gene may be a good marker for CNS or other cancers and would potentially serve as a good drug target for the treatment of certain cancers. This gene is also well expressed in several metabolic tissues (specifically adipose, liver and pancreas) and may thus have application for the treatment of metabolic diseases such as diabetes and obesity. Of particular interest is the good expression (CT value = 30.6) in pancreas. The human pancreas-specific gene SEL-11 is thought to be a negative regulator of the notch receptor (Harada, Y. et al. J Hum Genet 44(5):330-6, 1999). Thus, the notch-like MOL1a gene and notch receptor may have potential therapeutic use in diseases involving the pancreas.

Panel 1.3D Summary: Ag267 Among normal tissues, highest MOL1a transcript levels are found in adipose (CT value = 30). As was seen for Panels 1 and 1.2, moderate expression of this gene is detected in most regions of normal brain and the gene is strikingly over expressed in a number of CNS cancer cell lines. In general, expression of the MOL1a gene appears to be higher in cell lines when compared to tissue samples. A cluster of expression associated with brain, breast and renal cancer cell lines is evident. Thus, the expression of this gene could be associated with cancer cells when compared to normal, since these cell lines are derived from cancers. Alternatively, the expression of this gene could be associated with cell division, since a high percentage of cells in culture are actively dividing when compared to cells in tissue.

Panel 2D Summary: Ag267 Expression of the MOL1a gene in panel 2D appears to be widespread across most of the samples. However, there seems to be significant dysregulation in breast cancers when compared to normal adjacent tissues. Thus, therapeutic modulation of this gene might show utility in the treatment of breast cancers.

Panel 2.2 Summary: Ag1308 The expression of this gene appears to be widespread across most of the samples in panel 2.2. In a couple of instances of renal cell cancer, there seems to be significant dysregulation of the expression of this gene when compared to normal adjacent tissue. Thus, therapeutic modulation of this gene might be useful in the treatment of a sub-set of renal cancers.

Panel 4D Summary: Ag267/Ag1308 The MOL1a transcript is broadly expressed in fibroblasts, keratinocytes, B cells, and T cells, although at a moderate level. High expression of the transcript is also found in monocytes, whether activated or not. In addition, the transcript is up-regulated (7 fold) in keratinocytes and small airway epithelium by treatment with TNF α and IL-1. The Notch-like protein encoded by the MOL1a gene may regulate cell

survival based on its homology to other Notch proteins. Therefore, protein therapeutics (agonist or antagonists) against the MOL1a gene product may be beneficial in the treatment of lung diseases, such as asthma and emphysema, or in the treatment of skin diseases, such as psoriasis and contact sensitivity.

5

B. MOL2

Expression of gene MOL2 was assessed using the primer-probe set Ag2120, described in Table 17. Results of the RTQ-PCR runs are shown in Tables 18, 19, 20, and 21

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Table 17. Probe Name Ag2120

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-GCTGATTGCAAGAAGATGTTTC-3'	59	22	103	71
Probe	TET-5'-TTTTGTCAGCCCTGATTTCTTCGACA-3'-TAMRA	68.8	26	140	72
Reverse	5'-CCGATATGTCAGAATCTGCATT-3'	59.1	22	166	73

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Table 18. Panel 1.3D

Tissue Name	Relative Expression(%) 1.3Dtm3025t_ ag2120	Relative Expression(%) 1.3dtm3058t_ ag2120
Liver adenocarcinoma	0.5	0.1
Pancreas	0.3	0.2
Pancreatic ca. CAPAN 2	1.0	1.1
Adrenal gland	12.8	10.8
Thyroid	2.1	1.3
Salivary gland	0.6	1.1
Pituitary gland	0.6	0.3
Brain (fetal)	7.9	8.8
Brain (whole)	26.8	23.8
Brain (amygdala)	27.5	17.8
Brain (cerebellum)	17.4	19.2
Brain (hippocampus)	64.6	58.6
Brain (substantia nigra)	2.2	3.5
Brain (thalamus)	3.6	3.0
Cerebral Cortex	100.0	100.0

Spinal cord	0.5	1.2
CNS ca. (glio/astro) U87-MG	0.8	0.5
CNS ca. (glio/astro) U-118-MG	3.2	4.7
CNS ca. (astro) SW1783	0.7	0.8
CNS ca.* (neuro; met) SK-N-AS	0.4	0.2
CNS ca. (astro) SF-539	0.4	0.3
CNS ca. (astro) SNB-75	0.5	0.2
CNS ca. (glio) SNB-19	0.4	1.2
CNS ca. (glio) U251	1.6	1.3
CNS ca. (glio) SF-295	1.9	0.8
Heart (fetal)	3.3	2.2
Heart	0.3	0.6
Fetal Skeletal	6.8	9.3
Skeletal muscle	3.4	4.0
Bone marrow	0.9	1.6
Thymus	0.9	0.5
Spleen	0.4	0.0
Lymph node	1.2	0.6
Colorectal	1.6	1.1
Stomach	1.0	0.2
Small intestine	0.2	2.0
Colon ca. SW480	0.8	1.6
Colon ca.* (SW480 met)SW620	0.0	1.4
Colon ca. HT29	0.2	0.5
Colon ca. HCT-116	0.3	0.2
Colon ca. CaCo-2	0.6	0.0
83219 CC Well to Mod Diff (ODO3866)	1.5	0.5
Colon ca. HCC-2998	0.6	0.3
Gastric ca.* (liver met) NCI-N87	0.5	1.2
Bladder	1.8	1.0
Trachea	0.6	1.3
Kidney	1.3	2.5
Kidney (fetal)	1.7	4.0
Renal ca. 786-0	3.8	3.7
Renal ca. A498	2.6	3.0
Renal ca. RXF 393	2.2	2.3
Renal ca. ACHN	1.1	0.8
Renal ca. UO-31	0.5	1.2
Renal ca. TK-10	3.7	3.6
Liver	0.8	0.0
Liver (fetal)	0.2	0.0
Liver ca. (hepatoblast) HepG2	0.7	0.8
Lung	0.2	0.7
Lung (fetal)	0.4	0.6
Lung ca. (small cell) LX-1	1.2	0.1

Lung ca. (small cell) NCI-H69	44.8	40.9
Lung ca. (s.cell var.) SHP-77	5.6	5.2
Lung ca. (large cell) NCI-H460	54.3	74.2
Lung ca. (non-sm. cell) A549	0.5	0.0
Lung ca. (non-s.cell) NCI-H23	1.5	2.0
Lung ca (non-s.cell) HOP-62	7.0	5.3
Lung ca. (non-s.cl) NCI-H522	1.1	0.0
Lung ca. (squam.) SW 900	0.3	0.8
Lung ca. (squam.) NCI-H596	8.4	11.1
Mammary gland	2.4	2.0
Breast ca.* (pl. effusion) MCF-7	1.0	0.7
Breast ca.* (pl.ef) MDA-MB-231	0.0	0.0
Breast ca.* (pl. effusion) T47D	17.3	18.7
Breast ca. BT-549	4.2	4.7
Breast ca. MDA-N	9.3	9.9
Ovary	12.4	9.9
Ovarian ca. OVCAR-3	0.1	0.0
Ovarian ca. OVCAR-4	0.5	2.7
Ovarian ca. OVCAR-5	0.9	0.9
Ovarian ca. OVCAR-8	2.1	4.0
Ovarian ca. IGROV-1	0.4	0.3
Ovarian ca.* (ascites) SK-OV-3	0.8	0.0
Uterus	1.2	0.7
Placenta	1.8	0.1
Prostate	0.5	0.6
Prostate ca.* (bone met) PC-3	3.1	2.2
Testis	1.2	1.3
Melanoma Hs688(A).T	0.8	0.9
Melanoma* (met) Hs688(B).T	1.2	2.7
Melanoma UACC-62	0.7	0.7
Melanoma M14	4.0	5.5
Melanoma LOX IMVI	1.6	0.3
Melanoma* (met) SK-MEL-5	4.2	3.7
Adipose	3.1	1.9

Table 19. Panel 2D

Tissue Name	Relative Expression(%)	
	2Dtm3026t_ ag2120	2Dtm3035t_ ag2120
Normal Colon GENPAK 061003	7.3	7.4
83219 CC Well to Mod Diff (ODO3866)	4.3	7.9
83220 CC NAT (ODO3866)	1.7	2.9

83221 CC Gr.2 rectosigmoid (ODO3868)	2.3	1.5
83222 CC NAT (ODO3868)	1.7	3.8
83235 CC Mod Diff (ODO3920)	0.2	0.9
83236 CC NAT (ODO3920)	0.1	2.5
83237 CC Gr.2 ascend colon (ODO3921)	0.5	0.4
83238 CC NAT (ODO3921)	5.8	6.4
83241 CC from Partial Hepatectomy (ODO4309)	6.1	8.7
83242 Liver NAT (ODO4309)	4.0	2.2
87472 Colon mets to lung (OD04451-01)	0.0	0.3
87473 Lung NAT (OD04451-02)	2.9	3.9
Normal Prostate Clontech A+ 6546-1	3.0	7.8
84140 Prostate Cancer (OD04410)	8.5	9.0
84141 Prostate NAT (OD04410)	23.5	21.5
87073 Prostate Cancer (OD04720-01)	7.3	7.1
87074 Prostate NAT (OD04720-02)	1.7	11.3
Normal Lung GENPAK 061010	9.2	7.2
83239 Lung Met to Muscle (ODO4286)	0.7	0.7
83240 Muscle NAT (ODO4286)	11.3	12.5
84136 Lung Malignant Cancer (OD03126)	7.9	4.7
84137 Lung NAT (OD03126)	6.4	7.5
84871 Lung Cancer (OD04404)	3.0	3.8
84872 Lung NAT (OD04404)	2.6	2.8
84875 Lung Cancer (OD04565)	1.8	3.4
84876 Lung NAT (OD04565)	3.6	2.8
85950 Lung Cancer (OD04237-01)	22.5	17.3
85970 Lung NAT (OD04237-02)	3.5	4.5
83255 Ocular Mel Met to Liver (ODO4310)	2.1	4.1
83256 Liver NAT (ODO4310)	1.2	1.2
84139 Melanoma Mets to Lung (OD04321)	2.5	1.7
84138 Lung NAT (OD04321)	5.3	3.3
Normal Kidney GENPAK 061008	93.3	100.0
83786 Kidney Ca, Nuclear grade 2 (OD04338)	55.9	92.7
83787 Kidney NAT (OD04338)	37.9	36.6
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	67.4	76.3
83789 Kidney NAT (OD04339)	25.3	33.2
83790 Kidney Ca, Clear cell type (OD04340)	52.5	43.5
83791 Kidney NAT (OD04340)	0.0	35.6
83792 Kidney Ca, Nuclear grade 3 (OD04348)	5.0	7.6
83793 Kidney NAT (OD04348)	20.7	26.6
87474 Kidney Cancer (OD04622-01)	9.3	7.3
87475 Kidney NAT (OD04622-03)	7.1	10.2
85973 Kidney Cancer (OD04450-01)	27.0	29.3
85974 Kidney NAT (OD04450-03)	34.2	33.7
Kidney Cancer Clontech 8120607	4.1	3.3
Kidney NAT Clontech 8120608	9.2	12.8

Kidney Cancer Clontech 8120613	2.2	3.3
Kidney NAT Clontech 8120614	7.3	14.9
Kidney Cancer Clontech 9010320	22.4	26.4
Kidney NAT Clontech 9010321	18.3	26.8
Normal Uterus GENPAK 061018	9.6	8.6
Uterus Cancer GENPAK 064011	2.7	2.6
Normal Thyroid Clontech A+ 6570-1	5.1	5.3
Thyroid Cancer GENPAK 064010	39.2	44.1
Thyroid Cancer INVITROGEN A302152	30.8	24.5
Thyroid NAT INVITROGEN A302153	3.3	3.6
Normal Breast GENPAK 061019	5.0	4.5
84877 Breast Cancer (OD04566)	0.8	1.7
85975 Breast Cancer (OD04590-01)	9.7	7.6
85976 Breast Cancer Mets (OD04590-03)	26.1	33.4
87070 Breast Cancer Metastasis (OD04655-05)	3.4	4.1
GENPAK Breast Cancer 064006	3.3	4.4
Breast Cancer Res. Gen. 1024	7.2	8.3
Breast Cancer Clontech 9100266	3.1	3.7
Breast NAT Clontech 9100265	3.3	3.9
Breast Cancer INVITROGEN A209073	8.2	8.9
Breast NAT INVITROGEN A2090734	16.2	11.6
Normal Liver GENPAK 061009	1.4	0.9
Liver Cancer GENPAK 064003	1.8	5.1
Liver Cancer Research Genetics RNA 1025	1.3	2.0
Liver Cancer Research Genetics RNA 1026	3.4	2.4
Paired Liver Cancer Tissue Research Genetics RNA 6004-T	1.6	0.4
Paired Liver Tissue Research Genetics RNA 6004-N	1.3	1.0
Paired Liver Cancer Tissue Research Genetics RNA 6005-T	0.0	6.5
Paired Liver Tissue Research Genetics RNA 6005-N	1.6	0.3
Normal Bladder GENPAK 061001	3.4	9.5
Bladder Cancer Research Genetics RNA 1023	10.7	6.5
Bladder Cancer INVITROGEN A302173	1.8	2.1
87071 Bladder Cancer (OD04718-01)	1.7	5.2
87072 Bladder Normal Adjacent (OD04718-03)	4.2	6.3
Normal Ovary Res. Gen.	9.5	7.4
Ovarian Cancer GENPAK 064008	100.0	95.3
87492 Ovary Cancer (OD04768-07)	4.6	7.6
87493 Ovary NAT (OD04768-08)	7.3	5.7
Normal Stomach GENPAK 061017	1.7	3.8
Gastric Cancer Clontech 9060358	2.1	0.5
NAT Stomach Clontech 9060359	1.6	3.1
Gastric Cancer Clontech 9060395	3.3	3.1
NAT Stomach Clontech 9060394	2.2	3.3
Gastric Cancer Clontech 9060397	11.0	14.5
NAT Stomach Clontech 9060396	2.8	4.3

Gastric Cancer GENPAK 064005	2.2	6.5
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Table 20. Panel 4D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	4Dtm3027t_ ag2120		4Dtm3027t_ ag2120
93768_Secondary Th1_anti-CD28/anti-CD3	0.4	93100_HUVEC (Endothelial)_IL-1b	11.2
93769_Secondary Th2_anti-CD28/anti-CD3	0.8	93779_HUVEC (Endothelial)_IFN gamma	10.1
93770_Secondary Tr1_anti-CD28/anti-CD3	3.1	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	4.1
93573_Secondary Th1_resting day 4-6 in IL-2	3.4	93101_HUVEC (Endothelial)_TNF alpha + IL4	13.2
93572_Secondary Th2_resting day 4-6 in IL-2	1.5	93781_HUVEC (Endothelial)_IL-11	8.1
93571_Secondary Tr1_resting day 4-6 in IL-2	1.5	93583_Lung Microvascular Endothelial Cells_none	3.2
93568_primary Th1_anti-CD28/anti-CD3	0.3	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	2.4
93569_primary Th2_anti-CD28/anti-CD3	0.8	92662_Microvascular Dermal endothelium_none	0.0
93570_primary Tr1_anti-CD28/anti-CD3	0.4	92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93565_primary Th1_resting dy 4-6 in IL-2	3.1	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	3.1
93566_primary Th2_resting dy 4-6 in IL-2	5.5	93347_Small Airway Epithelium_none	5.4
93567_primary Tr1_resting dy 4-6 in IL-2	0.6	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	3.0
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	1.3	92668_Coronary Artery SMC_resting	35.6
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	2.4	92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	39.0
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	2.2	93107_astrocytes_resting	1.1
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	4.8	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.9
93574_chronic CD8 Lymphocytes 2ry_activated	2.4	92666_KU-812 (Basophil)_resting	0.5

CD3/CD28			
93354_CD4_none	0.9	92667_KU-812 (Basophil)_PMA/ionomycin	2.0
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0.7	93579_CCD1106 (Keratinocytes)_none	0.9
93103_LAK cells_resting	7.2	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	2.6
93788_LAK cells_IL-2	0.4	93791_Liver Cirrhosis	5.5
93787_LAK cells_IL-2+IL-12	2.8	93792_Lupus Kidney	9.3
93789_LAK cells_IL-2+IFN gamma	7.7	93577_NCI-H292	2.0
93790_LAK cells_IL-2+ IL-18	4.1	93358_NCI-H292_IL-4	5.3
93104_LAK cells_PMA/ionomycin and IL- 18	3.2	93360_NCI-H292_IL-9	3.8
93578_NK Cells IL-2_resting	2.3	93359_NCI-H292_IL-13	1.3
93109_Mixed Lymphocyte Reaction_Two Way MLR	2.7	93357_NCI-H292_IFN gamma	3.4
93110_Mixed Lymphocyte Reaction_Two Way MLR	4.0	93777_HPAEC_-	9.0
93111_Mixed Lymphocyte Reaction_Two Way MLR	5.2	93778_HPAEC_IL-1 beta/TNA alpha	15.4
93112_Mononuclear Cells (PBMCs)_resting	6.4	93254_Normal Human Lung Fibroblast_none	1.7
93113_Mononuclear Cells (PBMCs)_PWM	5.2	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.0
93114_Mononuclear Cells (PBMCs)_PHA-L	1.8	93257_Normal Human Lung Fibroblast_IL-4	2.8
93249_Ramos (B cell)_none	3.9	93256_Normal Human Lung Fibroblast_IL-9	1.6
93250_Ramos (B cell)_ionomycin	1.6	93255_Normal Human Lung Fibroblast_IL-13	1.0
93349_B lymphocytes_PWM	0.0	93258_Normal Human Lung Fibroblast_IFN gamma	1.4
93350_B lymphocytes_CD40L and IL-4	3.2	93106_Dermal Fibroblasts CCD1070_resting	0.6
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	67.4	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	2.3
93248_EOL-1 (Eosinophil)_dbcAMP/PMAion omycin	56.6	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	5.4
93356_Dendritic Cells_none	6.0	93772_dermal fibroblast_IFN gamma	0.5
93355_Dendritic Cells_LPS 100 ng/ml	15.5	93771_dermal fibroblast_IL-4	3.0
93775_Dendritic Cells_anti- CD40	13.5	93259_IBD Colitis 1**	1.3
93774_Monocytes_resting	46.0	93260_IBD Colitis 2	5.8
93776_Monocytes_LPS 50	4.9	93261_IBD Crohns	4.2

ng/ml			
93581_Macrophages_resting	47.3	735010_Colon_normal	5.8
93582_Macrophages_LPS 100 ng/ml	24.8	735019_Lung_none	7.0
93098_HUVEC (Endothelial)_none	10.2	64028-1_Thymus_none	100.0
93099_HUVEC (Endothelial)_starved	23.8	64030-1_Kidney_none	18.2

Table 21. Panel CNSD.01

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	CNS1x4tm618 4t ag2120 a2		CNS1x4tm618 4t ag2120 a2
102633_BA4 Control	46.5	102605_BA17 PSP	20.1
102641_BA4 Control2	42.9	102612_BA17 PSP2	10.5
102625_BA4 Alzheimer's2	5.2	102637_Sub Nigra Control	10.6
102649_BA4 Parkinson's	38.5	102645_Sub Nigra Control2	29.1
102656_BA4 Parkinson's2	100.0	102629_Sub Nigra Alzheimer's2	5.8
102664_BA4 Huntington's	53.8	102660_Sub Nigra Parkinson's2	20.6
102671_BA4 Huntington's2	4.3	102667_Sub Nigra Huntington's	21.5
102603_BA4 PSP	4.5	102674_Sub Nigra Huntington's2	14.7
102610_BA4 PSP2	14.1	102614_Sub Nigra PSP2	3.6
102588_BA4 Depression	11.8	102592_Sub Nigra Depression	3.2
102596_BA4 Depression2	3.5	102599_Sub Nigra Depression2	2.4
102634_BA7 Control	45.6	102636_Glob Palladus Control	1.8
102642_BA7 Control2	37.9	102644_Glob Palladus Control2	7.8
102626_BA7 Alzheimer's2	8.5	102620_Glob Palladus Alzheimer's	6.4
102650_BA7 Parkinson's	11.7	102628_Glob Palladus Alzheimer's2	2.5
102657_BA7 Parkinson's2	54.6	102652_Glob Palladus Parkinson's	34.4
102665_BA7 Huntington's	41.1	102659_Glob Palladus Parkinson's2	3.1
102672_BA7 Huntington's2	34.3	102606_Glob Palladus PSP	5.2
102604_BA7 PSP	36.2	102613_Glob Palladus PSP2	0.0
102611_BA7 PSP2	21.2	102591_Glob Palladus Depression	3.7
102589_BA7 Depression	4.5	102638_Temp Pole Control	11.0
102632_BA9 Control	18.1	102646_Temp Pole Control2	40.1
102640_BA9 Control2	76.7	102622_Temp Pole Alzheimer's	2.7
102617_BA9 Alzheimer's	8.0	102630_Temp Pole	3.4

		Alzheimer's2	
102624_BA9 Alzheimer's2	4.6	102653_Temp Pole Parkinson's	13.9
102648_BA9 Parkinson's	28.7	102661_Temp Pole Parkinson's2	20.8
102655_BA9 Parkinson's2	55.5	102668_Temp Pole Huntington's	27.6
102663_BA9 Huntington's	34.2	102607_Temp Pole PSP	2.5
102670_BA9 Huntington's2	4.7	102615_Temp Pole PSP2	3.7
102602_BA9 PSP	11.6	102600_Temp Pole Depression2	1.8
102609_BA9 PSP2	3.8	102639_Cing Gyr Control	70.7
102587_BA9 Depression	5.0	102647_Cing Gyr Control2	23.9
102595_BA9 Depression2	3.2	102623_Cing Gyr Alzheimer's	13.8
102635_BA17 Control	37.0	102631_Cing Gyr Alzheimer's2	7.8
102643_BA17 Control2	62.0	102654_Cing Gyr Parkinson's	13.2
102627_BA17 Alzheimer's2	2.9	102662_Cing Gyr Parkinson's2	23.0
102651_BA17 Parkinson's	13.4	102669_Cing Gyr Huntington's	40.3
102658_BA17 Parkinson's2	61.3	102676_Cing Gyr Huntington's2	12.9
102666_BA17 Huntington's	28.0	102608_Cing Gyr PSP	7.6
102673_BA17 Huntington's2	8.4	102616_Cing Gyr PSP2	5.6
102590_BA17 Depression	2.3	102594_Cing Gyr Depression	4.1
102597_BA17 Depression2	10.1	102601_Cing Gyr Depression2	4.6

Panel 1.3D Summary: Ag2120 Two replicate experiments using the same probe and primer set show very comparable results. Expression of the MOL2 gene is highest in the cerebral cortex (CT value = 29). Moderate expression is detected in all other regions of the brain except thalamus and substantia nigra; this observation suggests that the MOL2 gene may be associated with normal brain homeostasis. Thus, this protein shows a brain-preferential expression; see write-up on Panel CNS.01 for discussion of utility. In addition, expression of the MOL2 gene appears to be down-regulated in CNS cancer cell lines. Overexpression of the MOL2 gene is also detected in several lung cancer cell lines relative to normal control. Therefore, this gene might be a good target for the detection or treatment of CNS and lung cancers.

Panel 2D Summary: Ag2120 Two replicate experiments using the same probe and primer set show very comparable results. Expression of the MOL2 gene in panel 2D reveals an association of expression in thyroid, breast and kidney cancers when compared to their respective normal adjacent tissues. Thus, therapeutic modulation of this gene with inhibitory monoclonal antibodies and/or small molecule therapeutics may show utility in treatment of

these diseases. In addition, the MOL2 gene might be useful as a marker for thyroid, breast and kidney cancers.

Panel 4D Summary: Ag 2120 The MOL2 gene is expressed at highest levels in the thymus (CT value =31). In addition, the transcript is also expressed in eosinophils, monocytes, macrophages and coronary artery. Interestingly, it is down regulated in LPS-treated monocytes and to a lesser degree in LPS treated macrophages. Therefore, protein therapeutics (agonists or antagonists) designed against the protein encoded for by this transcript could reduce inflammatory process observed in asthma, emphysema, osteoarthritis and sepsis.

Panel CNSD.01 Summary: Ag2120 The insulin and insulin-like growth factors belong to a family of polypeptides essential for proper regulation of physiologic processes such as energy metabolism, cell proliferation, development, and differentiation. The insulin-like growth factors bind to IGF with high affinity and compete with the IGF receptor for IGF binding. Transgenic mice overexpressing insulin-like growth factor binding proteins (IGFBPs) tend to show brain developmental abnormalities, suggesting a role for these proteins in neurodevelopment. Furthermore, treatment with glycosaminoglycans (which increases muscle re-innervation after motor neuron death) upregulates serum levels of both IGF and IGFBP. Thus, the novel IGFBP encoded by the MOL2 gene may be useful in the treatment of diseases such as ALS, multiple sclerosis, and peripheral nerve injury on the basis of its homology to other established IGFBPs. The expression profile of this gene suggests that it is expressed preferentially in the brain, with highest levels in the cerebral cortex and hippocampus, two regions that are known to degenerate in Alzheimer's disease. Examination of the expression profile on Panel CNS.01 shows that most regions of both control and diseased brains express this protein; however the levels are decreased in the motor cortex in progressive supranuclear palsy and depression. Thus, this protein may additionally be of use in the treatment of Alzheimer's disease, progressive supranuclear palsy, and depression.

C. MOL3a

Expression of gene MOL3a was assessed using the primer-probe set Ag1493, described in Table 22. Results of the RTQ-PCR runs are shown in Tables 23, 24, 25, and 26.

Table 22. Probe Name Ag1493

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-GTGAAATCTGGCGTGGAGTATA-3'	59.1	22	1224	74
Probe	FAM-5'-CCTTGATGGGCACAGCCATCTTG-3'-TAMRA	70	23	1274	75
Reverse	5'-GTACTGGTTCCTCCAGGTACATGA-3'	58.8	22	1318	76

Table 23. Panel 1.2

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	1.2tm2058f_ag1493		1.2tm2058f_ag1493
Endothelial cells	0.2	Renal ca. 786-0	0.0
Endothelial cells (treated)	2.4	Renal ca. A498	0.5
Pancreas	0.1	Renal ca. RXF 393	0.9
Pancreatic ca. CAPAN 2	0.1	Renal ca. ACHN	0.2
Adrenal Gland (new lot*)	2.6	Renal ca. UO-31	1.3
Thyroid	1.0	Renal ca. TK-10	0.8
Salivary gland	21.8	Liver	1.4
Pituitary gland	0.4	Liver (fetal)	2.3
Brain (fetal)	3.3	Liver ca. (hepatoblast) HepG2	0.7
Brain (whole)	2.1	Lung	0.8
Brain (amygdala)	8.0	Lung (fetal)	1.0
Brain (cerebellum)	0.3	Lung ca. (small cell) LX-1	0.4
Brain (hippocampus)	15.0	Lung ca. (small cell) NCI-H69	1.9
Brain (thalamus)	3.5	Lung ca. (s.cell var.) SHP-77	0.0
Cerebral Cortex	30.1	Lung ca. (large cell) NCI-H460	0.7
Spinal cord	0.2	Lung ca. (non-sm. cell) A549	1.0
CNS ca. (glio/astro) U87-MG	0.2	Lung ca. (non-s.cell) NCI-H23	0.2
CNS ca. (glio/astro) U-118-MG	0.3	Lung ca. (non-s.cell) HOP-62	1.8
CNS ca. (astro) SW1783	0.0	Lung ca. (non-s.cl) NCI-H522	11.9
CNS ca.* (neuro; met) SK-N-AS	0.5	Lung ca. (squam.) SW 900	0.8
CNS ca. (astro) SF-539	0.4	Lung ca. (squam.) NCI-H596	1.0
CNS ca. (astro) SNB-75	0.1	Mammary gland	2.5
CNS ca. (glio) SNB-19	0.4	Breast ca.* (pl. effusion) MCF-7	3.7
CNS ca. (glio) U251	0.2	Breast ca.* (pl.ef) MDA-MB-231	0.0
CNS ca. (glio) SF-295	1.3	Breast ca.* (pl. effusion) T47D	17.6
Heart	5.1	Breast ca. BT-549	0.2
Skeletal Muscle (new lot*)	8.0	Breast ca. MDA-N	0.4
Bone marrow	15.6	Ovary	2.7
Thymus	1.2	Ovarian ca. OVCAR-3	8.3
Spleen	10.4	Ovarian ca. OVCAR-4	16.6

Lymph node	0.7	Ovarian ca. OVCAR-5	5.1
Colorectal	0.9	Ovarian ca. OVCAR-8	0.8
Stomach	2.9	Ovarian ca. IGROV-1	70.7
Small intestine	4.7	Ovarian ca.* (ascites) SK-OV-3	0.7
Colon ca. SW480	0.2	Uterus	0.6
Colon ca.* (SW480 met)SW620	0.0	Placenta	0.6
Colon ca. HT29	2.3	Prostate	27.9
Colon ca. HCT-116	0.0	Prostate ca.* (bone met)PC-3	0.3
Colon ca. CaCo-2	0.0	Testis	0.6
83219 CC Well to Mod Diff (ODO3866)	1.4	Melanoma Hs688(A).T	0.2
Colon ca. HCC-2998	2.8	Melanoma* (met) Hs688(B).T	0.4
Gastric ca.* (liver met) NCI-N87	1.6	Melanoma UACC-62	0.5
Bladder	6.9	Melanoma M14	0.1
Trachea	0.5	Melanoma LOX IMVI	0.1
Kidney	73.7	Melanoma* (met) SK-MEL-5	0.0
Kidney (fetal)	4.7	Adipose	100.0

Table 24. Panel 1.3D

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	1.3dx4tm5350f ag1493 b1		1.3dx4tm5350f ag1493 b1
Liver adenocarcinoma	1.2	Kidney (fetal)	18.7
Pancreas	0.0	Renal ca. 786-0	0.0
Pancreatic ca. CAPAN 2	1.9	Renal ca. A498	0.0
Adrenal gland	1.7	Renal ca. RXF 393	2.9
Thyroid	38.0	Renal ca. ACHN	1.0
Salivary gland	30.8	Renal ca. UO-31	0.8
Pituitary gland	4.5	Renal ca. TK-10	0.8
Brain (fetal)	48.3	Liver	0.4
Brain (whole)	60.7	Liver (fetal)	11.2
Brain (amygdala)	100.0	Liver ca. (hepatoblast) HepG2	0.6
Brain (cerebellum)	9.2	Lung	29.6
Brain (hippocampus)	68.2	Lung (fetal)	15.6
Brain (substantia nigra)	11.4	Lung ca. (small cell) LX-1	0.2
Brain (thalamus)	20.8	Lung ca. (small cell) NCI-H69	0.0
Cerebral Cortex	41.1	Lung ca. (s.cell var.) SHP-77	0.0
Spinal cord	10.0	Lung ca. (large cell)NCI-H460	0.5
CNS ca. (glio/astro) U87-MG	0.0	Lung ca. (non-sm. cell) A549	0.4
CNS ca. (glio/astro) U-118-MG	1.3	Lung ca. (non-s.cell) NCI-H23	0.0
CNS ca. (astro) SW1783	0.7	Lung ca (non-s.cell) HOP-62	2.6
CNS ca.* (neuro; met) SK-N-AS	1.9	Lung ca. (non-s.cl) NCI-H522	3.0

CNS ca. (astro) SF-539	0.5	Lung ca. (squam.) SW 900	0.2
CNS ca. (astro) SNB-75	0.4	Lung ca. (squam.) NCI-H596	0.0
CNS ca. (glio) SNB-19	0.4	Mammary gland	22.3
CNS ca. (glio) U251	1.2	Breast ca.* (pl. effusion) MCF-7	14.1
CNS ca. (glio) SF-295	0.6	Breast ca.* (pl.ef) MDA-MB-231	0.0
Heart (fetal)	1.3	Breast ca.* (pl. effusion) T47D	53.3
Heart	1.4	Breast ca. BT-549	0.5
Fetal Skeletal	4.2	Breast ca. MDA-N	0.0
Skeletal muscle	8.8	Ovary	2.1
Bone marrow	78.4	Ovarian ca. OVCAR-3	8.7
Thymus	3.9	Ovarian ca. OVCAR-4	25.1
Spleen	53.3	Ovarian ca. OVCAR-5	3.8
Lymph node	37.3	Ovarian ca. OVCAR-8	2.6
Colorectal	6.6	Ovarian ca. IGROV-1	29.2
Stomach	23.1	Ovarian ca.* (ascites) SK-OV-3	0.5
Small intestine	12.5	Uterus	8.9
Colon ca. SW480	0.0	Placenta	10.9
Colon ca.* (SW480 met)SW620	0.0	Prostate	50.9
Colon ca. HT29	2.9	Prostate ca.* (bone met)PC-3	0.0
Colon ca. HCT-116	0.0	Testis	18.7
Colon ca. CaCo-2	0.8	Melanoma Hs688(A).T	0.5
83219 CC Well to Mod Diff (ODO3866)	8.2	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	0.8	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	2.8	Melanoma M14	0.5
Bladder	5.3	Melanoma LOX IMVI	0.0
Trachea	35.6	Melanoma* (met) SK-MEL-5	0.0
Kidney	15.0	Adipose	60.2

Table 25. Panel 2D

Tissue Name	Relative Expression(%) 2Dtm2527f_ag 1493	Tissue Name	Relative Expression(%) 2Dtm2527f_ag 1493
Normal Colon GENPAK 061003	41.2	Kidney NAT Clontech 8120608	28.3
83219 CC Well to Mod Diff (ODO3866)	8.0	Kidney Cancer Clontech 8120613	10.7
83220 CC NAT (ODO3866)	9.3	Kidney NAT Clontech 8120614	46.0
83221 CC Gr.2 rectosigmoid (ODO3868)	5.1	Kidney Cancer Clontech 9010320	48.6
83222 CC NAT (ODO3868)	2.0	Kidney NAT Clontech 9010321	36.6
83235 CC Mod Diff	6.3	Normal Uterus GENPAK	8.4

(ODO3920)		061018	
83236 CC NAT (ODO3920)	4.4	Uterus Cancer GENPAK 064011	17.4
83237 CC Gr.2 ascend colon (ODO3921)	12.5	Normal Thyroid Clontech A+ 6570-1	100.0
83238 CC NAT (ODO3921)	6.1	Thyroid Cancer GENPAK 064010	39.8
83241 CC from Partial Hepatectomy (ODO4309)	17.0	Thyroid Cancer INVITROGEN A302152	28.3
83242 Liver NAT (ODO4309)	7.6	Thyroid NAT INVITROGEN A302153	44.4
87472 Colon mets to lung (OD04451-01)	16.6	Normal Breast GENPAK 061019	36.3
87473 Lung NAT (OD04451-02)	25.5	84877 Breast Cancer (OD04566)	24.7
Normal Prostate Clontech A+ 6546-1	82.4	85975 Breast Cancer (OD04590-01)	29.7
84140 Prostate Cancer (OD04410)	36.3	85976 Breast Cancer Mets (OD04590-03)	17.8
84141 Prostate NAT (OD04410)	47.0	87070 Breast Cancer Metastasis (OD04655-05)	79.6
87073 Prostate Cancer (OD04720-01)	36.1	GENPAK Breast Cancer 064006	25.9
87074 Prostate NAT (OD04720-02)	51.4	Breast Cancer Res. Gen. 1024	55.5
Normal Lung GENPAK 061010	41.8	Breast Cancer Clontech 9100266	24.0
83239 Lung Met to Muscle (ODO4286)	14.4	Breast NAT Clontech 9100265	13.7
83240 Muscle NAT (ODO4286)	4.5	Breast Cancer INVITROGEN A209073	29.1
84136 Lung Malignant Cancer (OD03126)	36.1	Breast NAT INVITROGEN A2090734	29.9
84137 Lung NAT (OD03126)	71.2	Normal Liver GENPAK 061009	1.0
84871 Lung Cancer (OD04404)	68.3	Liver Cancer GENPAK 064003	1.6
84872 Lung NAT (OD04404)	33.7	Liver Cancer Research Genetics RNA 1025	7.4
84875 Lung Cancer (OD04565)	25.5	Liver Cancer Research Genetics RNA 1026	4.3
84876 Lung NAT (OD04565)	18.4	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	8.5
85950 Lung Cancer (OD04237-01)	45.1	Paired Liver Tissue Research Genetics RNA 6004-N	10.1
85970 Lung NAT (OD04237-02)	55.1	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	7.5
83255 Ocular Mel Met to Liver (ODO4310)	8.7	Paired Liver Tissue Research Genetics RNA 6005-N	2.8
83256 Liver NAT (ODO4310)	4.7	Normal Bladder GENPAK 061001	11.7
84139 Melanoma Mets to Lung	4.0	Bladder Cancer Research	6.4

(OD04321)		Genetics RNA 1023	
84138 Lung NAT (OD04321)	50.3	Bladder Cancer INVITROGEN A302173	50.3
Normal Kidney GENPAK 061008	53.2	87071 Bladder Cancer (OD04718-01)	35.4
83786 Kidney Ca, Nuclear grade 2 (OD04338)	13.6	87072 Bladder Normal Adjacent (OD04718-03)	13.6
83787 Kidney NAT (OD04338)	54.0	Normal Ovary Res. Gen.	6.4
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	23.0	Ovarian Cancer GENPAK 064008	22.1
83789 Kidney NAT (OD04339)	26.6	87492 Ovary Cancer (OD04768-07)	29.3
83790 Kidney Ca, Clear cell type (OD04340)	31.0	87493 Ovary NAT (OD04768-08)	20.7
83791 Kidney NAT (OD04340)	49.7	Normal Stomach GENPAK 061017	21.9
83792 Kidney Ca, Nuclear grade 3 (OD04348)	7.8	Gastric Cancer Clontech 9060358	12.6
83793 Kidney NAT (OD04348)	35.8	NAT Stomach Clontech 9060359	33.7
87474 Kidney Cancer (OD04622-01)	17.8	Gastric Cancer Clontech 9060395	15.6
87475 Kidney NAT (OD04622-03)	15.4	NAT Stomach Clontech 9060394	51.8
85973 Kidney Cancer (OD04450-01)	1.7	Gastric Cancer Clontech 9060397	16.8
85974 Kidney NAT (OD04450-03)	43.2	NAT Stomach Clontech 9060396	12.4
Kidney Cancer Clontech 8120607	4.3	Gastric Cancer GENPAK 064005	12.9

Table 26. Panel 4.1D

Tissue Name	Relative Expression(%) 4.1dx4tm6520f ag1493_a1	Tissue Name	Relative Expression(%) 4.1dx4tm6520f ag1493_a1
93768_Secondary Th1_anti-CD28/anti-CD3	3.8	93100_HUVEC (Endothelial)_IL-1b	0.0
93769_Secondary Th2_anti-CD28/anti-CD3	27.0	93779_HUVEC (Endothelial)_IFN gamma	0.6
93770_Secondary Tr1_anti-CD28/anti-CD3	11.9	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	1.0
93573_Secondary Th1_resting day 4-6 in IL-2	1.1	93101_HUVEC (Endothelial)_TNF alpha + IL4	0.9
93572_Secondary Th2_resting day 4-6 in IL-2	3.2	93781_HUVEC (Endothelial)_IL-11	0.6
93571_Secondary Tr1_resting day 4-6 in IL-2	1.6	93583_Lung Microvascular Endothelial Cells_none	1.6
93568_primary Th1_anti-	6.7	93584_Lung Microvascular	0.6

CD28/anti-CD3		Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	
93569_primary Th2_anti-CD28/anti-CD3	8.4	92662_Microvascular Dermal endothelium_none	0.2
93570_primary Tr1_anti-CD28/anti-CD3	1.9	92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.3
93565_primary Th1_resting dy 4-6 in IL-2	0.4	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	2.1
93566_primary Th2_resting dy 4-6 in IL-2	0.7	93347_Small Airway Epithelium_none	1.0
93567_primary Tr1_resting dy 4-6 in IL-2	0.2	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	4.2
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	3.8	92668_Coronary Artery SMC_resting	0.1
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	7.1	92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.4
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	6.1	93107_astrocytes_resting	0.1
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	25.6	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	9.9	92666_KU-812 (Basophil)_resting	0.3
93354_CD4_none	0.5	92667_KU-812 (Basophil)_PMA/ionoycin	0.5
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	1.2	93579_CCD1106 (Keratinocytes)_none	4.2
93103_LAK cells_resting	25.6	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	4.0
93788_LAK cells_IL-2	3.2	93791_Liver Cirrhosis	1.7
93787_LAK cells_IL-2+IL-12	6.4	93577_NCI-H292	3.3
93789_LAK cells_IL-2+IFN gamma	5.3	93358_NCI-H292_IL-4	5.5
93790_LAK cells_IL-2+ IL-18	4.6	93360_NCI-H292_IL-9	4.6
93104_LAK cells_PMA/ionomycin and IL-18	11.6	93359_NCI-H292_IL-13	6.3
93578_NK Cells_IL-2_resting	3.0	93357_NCI-H292_IFN gamma	3.4
93109_Mixed Lymphocyte Reaction_Two Way MLR	17.2	93777_HPAEC_-	0.2
93110_Mixed Lymphocyte Reaction_Two Way MLR	13.5	93778_HPAEC_IL-1 beta/TNA alpha	0.5
93111_Mixed Lymphocyte Reaction_Two Way MLR	5.4	93254_Normal Human Lung Fibroblast_none	0.5
93112_Mononuclear Cells (PBMCs)_resting	9.1	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and	0.3

		IL-1b (1 ng/ml)	
93113_Mononuclear Cells (PBMCs) PWM	11.5	93257_Normal Human Lung Fibroblast IL-4	0.2
93114_Mononuclear Cells (PBMCs) PHA-L	20.5	93256_Normal Human Lung Fibroblast IL-9	0.3
93249_Ramos (B cell)_none	70.5	93255_Normal Human Lung Fibroblast IL-13	0.6
93250_Ramos (B cell)_ionomycin	100.0	93258_Normal Human Lung Fibroblast IFN gamma	0.5
93349_B lymphocytes PWM	12.4	93106_Dermal Fibroblasts CCD1070 resting	0.5
93350_B lymphocytes_CD40L and IL-4	64.9	93361_Dermal Fibroblasts CCD1070 TNF alpha 4 ng/ml	4.1
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	10.0	93105_Dermal Fibroblasts CCD1070 IL-1 beta 1 ng/ml	0.1
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	6.9	93772_dermal fibroblast_IFN gamma	1.0
93356_Dendritic Cells none	10.1	93771_dermal fibroblast IL-4	2.2
93355_Dendritic Cells_LPS 100 ng/ml	21.1	93892_Dermal fibroblasts none	1.0
93775_Dendritic Cells_anti-CD40	9.9	99202_Neutrophils TNFa+LPS	9.2
93774_Monocytes_resting	38.2	99203_Neutrophils none	38.1
93776_Monocytes_LPS 50 ng/ml	51.1	735010_Colon normal	1.2
93581_Macrophages_resting	18.4	735019_Lung none	5.5
93582_Macrophages_LPS 100 ng/ml	19.7	64028-1_Thymus none	8.2
93098_HUVEC (Endothelial)_none	0.0	64030-1_Kidney none	9.8
93099_HUVEC (Endothelial)_starved	0.3		

Table 27. Panel CNSD.01

Tissue Name	Relative Expression(%) cns1x4tm6179f ag1493 b1	Tissue Name	Relative Expression(%) cns1x4tm6179f ag1493 b1
102633_BA4 Control	14.8	102605_BA17 PSP	15.9
102641_BA4 Control2	51.1	102612_BA17 PSP2	8.3
102625_BA4 Alzheimer's2	3.6	102637_Sub Nigra Control	28.5
102649_BA4 Parkinson's	36.3	102645_Sub Nigra Control2	47.1
102656_BA4 Parkinson's2	54.3	102629_Sub Nigra Alzheimer's2	3.3
102664_BA4 Huntington's	17.2	102660_Sub Nigra Parkinson's2	61.6
102671_BA4 Huntington's2	4.3	102667_Sub Nigra Huntington's	37.6

102603 BA4 PSP	0.0	102674_Sub Nigra Huntington's2	8.2
102610 BA4 PSP2	14.0	102614 Sub Nigra PSP2	4.6
102588 BA4 Depression	14.9	102592 Sub Nigra Depression	6.8
102596 BA4 Depression2	2.6	102599 Sub Nigra Depression2	6.6
102634 BA7 Control	16.5	102636 Glob Palladus Control	10.2
102642 BA7 Control2	13.7	102644 Glob Palladus Control2	9.0
102626 BA7 Alzheimer's2	3.9	102620 Glob Palladus Alzheimer's	4.4
102650 BA7 Parkinson's	18.2	102628 Glob Palladus Alzheimer's2	2.6
102657 BA7 Parkinson's2	45.6	102652_Glob Palladus Parkinson's	80.4
102665 BA7 Huntington's	35.9	102659_Glob Palladus Parkinson's2	5.2
102672 BA7 Huntington's2	18.7	102606 Glob Palladus PSP	6.4
102604 BA7 PSP	54.8	102613 Glob Palladus PSP2	2.7
102611 BA7 PSP2	17.8	102591_Glob Palladus Depression	4.0
102589 BA7 Depression	11.2	102638 Temp Pole Control	13.8
102632 BA9 Control	16.1	102646 Temp Pole Control2	100.0
102640 BA9 Control2	96.5	102622 Temp Pole Alzheimer's	0.8
102617 BA9 Alzheimer's	0.0	102630 Temp Pole Alzheimer's2	3.0
102624 BA9 Alzheimer's2	7.0	102653 Temp Pole Parkinson's	51.3
102648 BA9 Parkinson's	29.5	102661 Temp Pole Parkinson's2	34.2
102655 BA9 Parkinson's2	47.8	102668 Temp Pole Huntington's	50.4
102663 BA9 Huntington's	27.6	102607 Temp Pole PSP	1.2
102670 BA9 Huntington's2	14.9	102615 Temp Pole PSP2	1.7
102602 BA9 PSP	9.0	102600 Temp Pole Depression2	8.9
102609 BA9 PSP2	3.1	102639 Cing Gyr Control	50.1
102587 BA9 Depression	3.2	102647 Cing Gyr Control2	55.7
102595 BA9 Depression2	5.3	102623 Cing Gyr Alzheimer's	18.9
102635 BA17 Control	17.9	102631 Cing Gyr Alzheimer's2	0.9
102643 BA17 Control2	37.2	102654 Cing Gyr Parkinson's	35.5
102627 BA17 Alzheimer's2	5.7	102662 Cing Gyr Parkinson's2	84.5
102651 BA17 Parkinson's	45.7	102669 Cing Gyr Huntington's	67.5
102658 BA17 Parkinson's2	18.1	102676_Cing Gyr Huntington's2	23.3
102666 BA17 Huntington's	15.1	102608 Cing Gyr PSP	14.0
102673 BA17 Huntington's2	13.0	102616 Cing Gyr PSP2	7.9
102590 BA17 Depression	9.4	102594 Cing Gyr Depression	3.0
102597 BA17 Depression2	31.9	102601 Cing Gyr Depression2	11.8

Panel 1.2 Summary: Ag1493 The high expression of the MOL3a gene seen in adipose (CT value = 25) is most likely skewed due to genomic DNA contamination in this sample. Otherwise, the gene is expressed mainly in normal tissues, including brain (particularly cerebral cortex), kidney, and prostate. Expression of the MOL3a gene in skeletal muscle and liver may suggest function in metabolic diseases, including obesity and diabetes. Furthermore, MOL3a expression is down regulated in a number of tumor cell lines relative to the normal controls suggesting a potential utility of this gene in the treatment of cancer.

Panel 1.3D Summary: Ag1493 In this panel, highest expression of the MOL3a gene is detected in the amygdala of the brain (CT value = 29.6). This may suggest that the MOL3a gene plays a role in normal brain function, including fear and anxiety response. In addition, high expression is also observed in adipose and bone marrow suggesting potential roles in metabolic and immune function. Overall, expression of the MOL3a gene in panel 1.3D reveals that it is associated mostly with normal tissues. In a couple of instances, the expression of this gene is seen in clusters of cell lines, specifically in breast and ovarian cancer cell lines. Thus, therapeutic modulation of expression of this gene may be of utility in the treatment breast and ovarian cancers. Alternatively, replacement of the MOL3a protein that is missing from some cancer cells using recombinant protein might provide a useful treatment for these types of cancers.

Panel 2D Summary: Ag1493 Expression of the MOL3a gene is highest in thyroid and appears to be widespread across many samples on Panel 2D. However, overall there appears to be generally higher expression in normal tissues when compared to cancerous counterparts. Thus, therapeutic modulation of this gene or gene product might show utility for a range of oncology indications. Semaphorins and their receptors are known signals for axon guidance; they are also suspected to regulate developmental processes involving cell migration and morphogenesis, and have been implicated in immune function and tumor progression.

Panel 4.1D Summary: Ag1493 The MOL3a transcript is highly expressed in a B cell line as well as in B cells stimulated with CD40L and IL4. Expression of this transcript is also found to a lesser degree in monocytes and macrophages independently of their activation status. Of interest, CD100, which is an activation molecule on T cells, is a member of the semaphorin protein family. The semaphorin B-like protein encoded by the MOL3a transcript could therefore also serve as a B cell activation marker. The semaphorin family has additionally been reported to play a role in chemotaxis. Thus, protein therapeutics or monoclonal antibodies raised against the MOL3a protein, could inhibit spontaneous and chemokine induced migration of B cells and monocytes and potentially regulate B cell

differentiation and B cell isotype switching. Regulation of this molecule by protein therapeutics or monoclonal antibodies could also function to regulate immunity and be important for the treatment of autoimmune diseases, allergic diseases, and immune rejection in transplantation. In support of this hypothesis, recent studies indicate that semaphorins bind with high affinity to at least two different receptor families and are biologically active on immune cells as well as neuronal cells (Curr Opin Immunol 1999 Aug;11(4):387-91).

Panel CNSD.01 Summary: Ag1493 Semaphorins can act as axon guidance proteins, specifically through their ability to act as chemorepellents that inhibit CNS regenerative capacity. Although there is considerable variance between individuals in MOL3a gene expression levels in this panel, levels of this protein are reduced to less than 1/3 of that seen in controls in the temporal cortex of Alzheimer's patients (which shows marked synaptogenic loss in mid to late phases of the disease) as well as in diseases not associated with neurodegeneration of the temporal cortex. Therefore, manipulation of levels of this protein may be of use in inducing a compensatory synaptogenic response to neuronal death in Alzheimer's disease.

D. MOL4

Expression of gene MOL4 was assessed using the primer-probe set Ag1216, described in Table 28. Results of the RTQ-PCR runs are shown in Tables 29, 30, 31, and 32.

Table 28. Probe Name: Ag1216

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-CCCGAAGAATGAAAAGTACACA-3'	59.1	22	5263	77
Probe	FAM-5'- CCCATGGAATTCAAGACCCTGAACAA-3'- TAMRA	69.7	26	5285	78
Reverse	5'-AATGGGTAGAAGTTGGCTCTGT-3'	59.2	22	5331	79

Table 29. Panel 1.2

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	1.2tm1404f_ ag1216		1.2tm1404f_ ag1216
Endothelial cells	0.0	Renal ca. 786-0	100.0

Endothelial cells (treated)	76.8	Renal ca. A498	3.0
Pancreas	11.3	Renal ca. RXF 393	45.4
Pancreatic ca. CAPAN 2	0.0	Renal ca. ACHN	0.2
Adrenal Gland (new lot*)	12.2	Renal ca. UO-31	0.0
Thyroid	11.6	Renal ca. TK-10	0.0
Salivary gland	2.7	Liver	7.5
Pituitary gland	12.6	Liver (fetal)	7.7
Brain (fetal)	77.9	Liver ca. (hepatoblast) HepG2	0.0
Brain (whole)	73.2	Lung	6.1
Brain (amygdala)	33.7	Lung (fetal)	13.1
Brain (cerebellum)	6.8	Lung ca. (small cell) LX-1	0.0
Brain (hippocampus)	75.3	Lung ca. (small cell) NCI-H69	0.0
Brain (thalamus)	9.9	Lung ca. (s.cell var.) SHP-77	0.0
Cerebral Cortex	87.7	Lung ca. (large cell) NCI-H460	0.0
Spinal cord	8.3	Lung ca. (non-sm. cell) A549	0.0
CNS ca. (glio/astro) U87-MG	0.0	Lung ca. (non-s.cell) NCI-H23	0.0
CNS ca. (glio/astro) U-118-MG	1.5	Lung ca. (non-s.cell) HOP-62	0.0
CNS ca. (astro) SW1783	0.0	Lung ca. (non-s.cl) NCI-H522	0.0
CNS ca.* (neuro; met) SK-N-AS	11.1	Lung ca. (squam.) SW 900	0.0
CNS ca. (astro) SF-539	0.0	Lung ca. (squam.) NCI-H596	0.0
CNS ca. (astro) SNB-75	6.4	Mammary gland	13.0
CNS ca. (glio) SNB-19	4.4	Breast ca.* (pl. effusion) MCF-7	0.0
CNS ca. (glio) U251	4.2	Breast ca.* (pl.ef) MDA-MB-231	0.0
CNS ca. (glio) SF-295	0.0	Breast ca.* (pl. effusion) T47D	0.0
Heart	61.1	Breast ca. BT-549	1.8
Skeletal Muscle (new lot*)	8.2	Breast ca. MDA-N	0.0
Bone marrow	0.1	Ovary	10.2
Thymus	0.2	Ovarian ca. OVCAR-3	66.4
Spleen	0.0	Ovarian ca. OVCAR-4	1.3
Lymph node	5.1	Ovarian ca. OVCAR-5	3.5
Colorectal	0.2	Ovarian ca. OVCAR-8	0.0
Stomach	5.9	Ovarian ca. IGROV-1	0.3
Small intestine	11.8	Ovarian ca.* (ascites) SK-OV-3	0.0
Colon ca. SW480	0.0	Uterus	7.7
Colon ca.* (SW480 met)SW620	2.7	Placenta	8.1
Colon ca. HT29	0.0	Prostate	4.6
Colon ca. HCT-116	0.0	Prostate ca.* (bone met)PC-3	0.0
Colon ca. CaCo-2	0.5	Testis	4.6
83219 CC Well to Mod Diff (ODO3866)	0.5	Melanoma Hs688(A).T	0.0
Colon ca. HCC-2998	0.0	Melanoma* (met) Hs688(B).T	0.0
Gastric ca.* (liver met) NCI-N87	0.0	Melanoma UACC-62	0.0
Bladder	6.7	Melanoma M14	0.0

Trachea	3.1	Melanoma LOX IMVI	0.0
Kidney	32.3	Melanoma* (met) SK-MEL-5	0.0
Kidney (fetal)	51.8	Adipose	1.5

Table 30. Panel 2.2

Tissue Name	Relative Expression(%) 2.2x4tm6515f_ ag1216 b1	Tissue Name	Relative Expression(%) 2.2x4tm6515f_ ag1216 b1
Normal Colon GENPAK 061003	0.1	83793 Kidney NAT (OD04348)	11.6
97759 Colon cancer (OD06064)	0.0	98938 Kidney malignant cancer (OD06204B)	0.0
97760 Colon cancer NAT (OD06064)	0.4	98939 Kidney normal adjacent tissue (OD06204E)	1.4
97778 Colon cancer (OD06159)	0.0	85973 Kidney Cancer (OD04450-01)	1.3
97779 Colon cancer NAT (OD06159)	0.8	85974 Kidney NAT (OD04450-03)	3.2
98861 Colon cancer (OD06297-04)	0.0	Kidney Cancer Clontech 8120613	0.0
98862 Colon cancer NAT (OD06297-015)	0.6	Kidney NAT Clontech 8120614	3.5
83237 CC Gr.2 ascend colon (ODO3921)	0.2	Kidney Cancer Clontech 9010320	3.5
83238 CC NAT (ODO3921)	0.0	Kidney NAT Clontech 9010321	0.9
97766 Colon cancer metastasis (OD06104)	0.2	Kidney Cancer Clontech 8120607	8.3
97767 Lung NAT (OD06104)	1.1	Kidney NAT Clontech 8120608	0.7
87472 Colon mets to lung (OD04451-01)	0.3	Normal Uterus GENPAK 061018	2.9
87473 Lung NAT (OD04451-02)	0.4	Uterus Cancer GENPAK 064011	0.2
Normal Prostate Clontech A+ 6546-1 (8090438)	0.5	Normal Thyroid Clontech A+ 6570-1 (7080817)	0.4
84140 Prostate Cancer (OD04410)	0.2	Thyroid Cancer GENPAK 064010	0.2
84141 Prostate NAT (OD04410)	0.0	Thyroid Cancer INVITROGEN A302152	0.3
Normal Ovary Res. Gen.	2.3	Thyroid NAT INVITROGEN A302153	0.3
98863 Ovarian cancer (OD06283-03)	4.6	Normal Breast GENPAK 061019	1.3
98865 Ovarian cancer NAT/fallopian tube (OD06283-07)	1.3	84877 Breast Cancer (OD04566)	0.4
Ovarian Cancer GENPAK 064008	9.7	Breast Cancer Res. Gen. 1024	0.4
97773 Ovarian cancer (OD06145)	0.0	85975 Breast Cancer (OD04590-01)	1.6

97775 Ovarian cancer NAT (OD06145)	0.0	85976 Breast Cancer Mets (OD04590-03)	0.8
98853 Ovarian cancer (OD06455-03)	0.2	87070 Breast Cancer Metastasis (OD04655-05)	0.6
98854 Ovarian NAT (OD06455-07) Fallopian tube	1.9	GENPAK Breast Cancer 064006	0.9
Normal Lung GENPAK 061010	0.6	Breast Cancer Clontech 9100266	1.4
92337 Invasive poor diff. lung adeno (ODO4945-01)	0.4	Breast NAT Clontech 9100265	0.6
92338 Lung NAT (ODO4945-03)	0.2	Breast Cancer INVITROGEN A209073	0.0
84136 Lung Malignant Cancer (OD03126)	0.0	Breast NAT INVITROGEN A2090734	1.4
84137 Lung NAT (OD03126)	0.4	97763 Breast cancer (OD06083)	0.8
90372 Lung Cancer (OD05014A)	1.0	97764 Breast cancer node metastasis (OD06083)	0.9
90373 Lung NAT (OD05014B)	2.1	Normal Liver GENPAK 061009	0.3
97761 Lung cancer (OD06081)	0.8	Liver Cancer Research Genetics RNA 1026	0.7
97762 Lung cancer NAT (OD06081)	0.4	Liver Cancer Research Genetics RNA 1025	1.6
85950 Lung Cancer (OD04237-01)	0.4	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	0.0
85970 Lung NAT (OD04237-02)	0.0	Paired Liver Tissue Research Genetics RNA 6004-N	0.0
83255 Ocular Mel Met to Liver (ODO4310)	0.2	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	1.3
83256 Liver NAT (ODO4310)	0.0	Paired Liver Tissue Research Genetics RNA 6005-N	0.4
84139 Melanoma Mets to Lung (OD04321)	0.7	Liver Cancer GENPAK 064003	0.5
84138 Lung NAT (OD04321)	0.0	Normal Bladder GENPAK 061001	0.8
Normal Kidney GENPAK 061008	1.7	Bladder Cancer Research Genetics RNA 1023	0.7
83786 Kidney Ca, Nuclear grade 2 (OD04338)	5.3	Bladder Cancer INVITROGEN A302173	0.2
83787 Kidney NAT (OD04338)	6.2	Normal Stomach GENPAK 061017	1.0
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	100.0	Gastric Cancer Clontech 9060397	0.2
83789 Kidney NAT (OD04339)	3.0	NAT Stomach Clontech 9060396	0.4
83790 Kidney Ca, Clear cell type (OD04340)	26.3	Gastric Cancer Clontech 9060395	0.4
83791 Kidney NAT (OD04340)	0.9	NAT Stomach Clontech 9060394	0.7
83792 Kidney Ca, Nuclear	5.1	Gastric Cancer GENPAK	1.1

grade 3 (OD04348)		064005	
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Table 31. Panel 4D

Tissue Name	Relative Expression(%)	
	4Dtm2072f_ ag1216	4Dtm2246f_ ag1216
93768 Secondary Th1 anti-CD28/anti-CD3	0.0	0.0
93769 Secondary Th2 anti-CD28/anti-CD3	0.0	0.0
93770 Secondary Tr1 anti-CD28/anti-CD3	0.0	0.0
93573 Secondary Th1 resting day 4-6 in IL-2	0.0	0.0
93572 Secondary Th2 resting day 4-6 in IL-2	0.0	0.0
93571 Secondary Tr1 resting day 4-6 in IL-2	0.0	0.0
93568 primary Th1 anti-CD28/anti-CD3	0.0	0.0
93569 primary Th2 anti-CD28/anti-CD3	0.0	0.0
93570 primary Tr1 anti-CD28/anti-CD3	0.0	0.0
93565 primary Th1 resting dy 4-6 in IL-2	0.0	0.0
93566 primary Th2 resting dy 4-6 in IL-2	1.1	0.0
93567 primary Tr1 resting dy 4-6 in IL-2	0.0	0.9
93351 CD45RA CD4 lymphocyte anti-CD28/anti-CD3	0.0	0.0
93352 CD45RO CD4 lymphocyte anti-CD28/anti-CD3	0.8	0.0
93251 CD8 Lymphocytes anti-CD28/anti-CD3	0.0	0.0
93353 chronic CD8 Lymphocytes 2ry resting dy 4-6 in IL-2	0.0	1.3
93574 chronic CD8 Lymphocytes 2ry activated CD3/CD28	0.0	0.0
93354 CD4 none	0.0	0.9
93252 Secondary Th1/Th2/Tr1 anti-CD95 CH11	0.0	0.0
93103 LAK cells resting	0.0	0.0
93788 LAK cells IL-2	0.0	0.0
93787 LAK cells IL-2+IL-12	0.0	1.9
93789 LAK cells IL-2+IFN gamma	1.1	0.0
93790 LAK cells IL-2+ IL-18	0.0	0.0
93104 LAK cells PMA/ionomycin and IL-18	0.0	0.0
93578 NK Cells IL-2 resting	0.0	0.0
93109 Mixed Lymphocyte Reaction Two Way MLR	0.0	0.0
93110 Mixed Lymphocyte Reaction Two Way MLR	0.0	0.0
93111 Mixed Lymphocyte Reaction Two Way MLR	0.0	0.0
93112 Mononuclear Cells (PBMCs) resting	0.0	0.0
93113 Mononuclear Cells (PBMCs) PWM	2.8	2.5
93114 Mononuclear Cells (PBMCs) PHA-L	0.0	3.1
93249 Ramos (B cell) none	0.0	0.0
93250 Ramos (B cell) ionomycin	0.0	0.0
93349 B lymphocytes PWM	0.0	0.0
93350 B lymphocytes CD40L and IL-4	1.1	0.0
92665 EOL-1 (Eosinophil) dbcAMP differentiated	0.0	0.0
93248 EOL-1 (Eosinophil) dbcAMP/PMAionomycin	0.0	0.0

93356_Dendritic Cells_none	0.0	0.0
93355_Dendritic Cells_LPS 100 ng/ml	0.0	0.0
93775_Dendritic Cells_anti-CD40	0.0	0.0
93774_Monocytes_resting	0.0	0.0
93776_Monocytes_LPS 50 ng/ml	0.0	0.0
93581_Macrophages_resting	0.0	0.0
93582_Macrophages_LPS 100 ng/ml	0.8	0.0
93098_HUVEC (Endothelial)_none	0.0	0.0
93099_HUVEC (Endothelial)_starved	0.0	0.0
93100_HUVEC (Endothelial)_IL-1b	0.0	1.3
93779_HUVEC (Endothelial)_IFN gamma	0.0	0.0
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.0	0.0
93101_HUVEC (Endothelial)_TNF alpha + IL4	0.0	0.0
93781_HUVEC (Endothelial)_IL-11	0.9	0.0
93583_Lung Microvascular Endothelial Cells_none	0.0	0.0
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
92662_Microvascular Dermal endothelium_none	0.0	0.0
92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	20.3	31.9
93347_Small Airway Epithelium_none	1.8	2.0
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	2.7	2.5
92668_Coronary Artery SMC_resting	0.0	0.0
92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
93107_astrocytes_resting	12.8	16.3
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	5.3	13.5
92666_KU-812 (Basophil)_resting	0.0	0.0
92667_KU-812 (Basophil)_PMA/ionoycin	0.0	0.0
93579_CCD1106 (Keratinocytes)_none	1.4	0.0
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	0.0	4.1
93791_Liver Cirrhosis	1.9	2.3
93792_Lupus Kidney	5.9	10.3
93577_NCI-H292	1.6	0.0
93358_NCI-H292_IL-4	0.7	0.0
93360_NCI-H292_IL-9	0.0	2.8
93359_NCI-H292_IL-13	0.0	0.0
93357_NCI-H292_IFN gamma	0.0	0.0
93777_HPAEC_-	0.0	0.0
93778_HPAEC_IL-1 beta/TNA alpha	0.0	0.0
93254_Normal Human Lung Fibroblast_none	0.0	0.0
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.0	0.0
93257_Normal Human Lung Fibroblast_IL-4	0.0	0.0

93256 Normal Human Lung Fibroblast IL-9	0.0	0.0
93255 Normal Human Lung Fibroblast IL-13	0.0	0.0
93258 Normal Human Lung Fibroblast IFN gamma	0.0	0.0
93106 Dermal Fibroblasts CCD1070 resting	0.0	0.0
93361 Dermal Fibroblasts CCD1070 TNF alpha 4 ng/ml	0.0	0.0
93105 Dermal Fibroblasts CCD1070 IL-1 beta 1 ng/ml	0.0	0.0
93772 dermal fibroblast IFN gamma	0.0	0.0
93771 dermal fibroblast IL-4	0.0	1.5
93259 IBD Colitis 1**	1.5	2.8
93260 IBD Colitis 2	0.0	1.2
93261 IBD Crohns	1.4	4.0
735010 Colon normal	3.4	2.7
735019 Lung none	52.1	42.3
64028-1 Thymus none	100.0	100.0
64030-1 Kidney none	1.6	0.0

Panel 32. Panel CNSD.01

Tissue Name	Relative Expression(%) cns1x4tm6177f ag1216 b2	Tissue Name	Relative Expression(%) cns1x4tm6177f ag1216 b2
102633 BA4 Control	18.7	102605 BA17 PSP	38.3
102641 BA4 Control2	62.0	102612 BA17 PSP2	19.2
102625 BA4 Alzheimer's2	17.2	102637 Sub Nigra Control	6.8
102649 BA4 Parkinson's	79.4	102645 Sub Nigra Control2	12.2
102656 BA4 Parkinson's2	54.7	102629 Sub Nigra Alzheimer's2	10.8
102664 BA4 Huntington's	37.5	102660 Sub Nigra Parkinson's2	17.4
102671 BA4 Huntington's2	17.0	102667 Sub Nigra Huntington's	21.1
102603 BA4 PSP	16.5	102674 Sub Nigra Huntington's2	8.6
102610 BA4 PSP2	22.9	102614 Sub Nigra PSP2	1.9
102588 BA4 Depression	45.0	102592 Sub Nigra Depression	1.9
102596 BA4 Depression2	27.0	102599 Sub Nigra Depression2	3.6
102634 BA7 Control	45.2	102636 Glob Palladus Control	21.2
102642 BA7 Control2	25.5	102644 Glob Palladus Control2	12.8
102626 BA7 Alzheimer's2	20.0	102620 Glob Palladus Alzheimer's	3.0
102650 BA7 Parkinson's	48.1	102628 Glob Palladus Alzheimer's2	4.2
102657 BA7 Parkinson's2	27.3	102652 Glob Palladus Parkinson's	100.0
102665 BA7 Huntington's	58.5	102659 Glob Palladus Parkinson's2	10.6
102672 BA7 Huntington's2	65.1	102606 Glob Palladus PSP	4.3

102604_BA7 PSP	93.8	102613_Glob Palladus PSP2	6.8
102611_BA7 PSP2	34.8	102591_Glob Palladus Depression	9.1
102589_BA7 Depression	20.9	102638_Temp Pole Control	29.7
102632_BA9 Control	35.4	102646_Temp Pole Control2	63.9
102640_BA9 Control2	58.7	102622_Temp Pole Alzheimer's	7.3
102617_BA9 Alzheimer's	9.2	102630_Temp Pole Alzheimer's2	16.4
102624_BA9 Alzheimer's2	36.1	102653_Temp Pole Parkinson's	88.4
102648_BA9 Parkinson's	33.0	102661_Temp Pole Parkinson's2	50.2
102655_BA9 Parkinson's2	32.2	102668_Temp Pole Huntington's	63.5
102663_BA9 Huntington's	50.4	102607_Temp Pole PSP	22.1
102670_BA9 Huntington's2	18.6	102615_Temp Pole PSP2	11.4
102602_BA9 PSP	14.3	102600_Temp Pole Depression2	36.9
102609_BA9 PSP2	7.6	102639_Cing Gyr Control	60.1
102587_BA9 Depression	14.9	102647_Cing Gyr Control2	48.0
102595_BA9 Depression2	18.3	102623_Cing Gyr Alzheimer's	19.4
102635_BA17 Control	87.9	102631_Cing Gyr Alzheimer's2	24.8
102643_BA17 Control2	73.0	102654_Cing Gyr Parkinson's	29.7
102627_BA17 Alzheimer's2	36.7	102662_Cing Gyr Parkinson's2	33.2
102651_BA17 Parkinson's	81.0	102669_Cing Gyr Huntington's	36.0
102658_BA17 Parkinson's2	95.4	102676_Cing Gyr Huntington's2	27.7
102666_BA17 Huntington's	78.7	102608_Cing Gyr PSP	20.7
102673_BA17 Huntington's2	37.6	102616_Cing Gyr PSP2	3.9
102590_BA17 Depression	33.7	102594_Cing Gyr Depression	34.6
102597_BA17 Depression2	73.7	102601_Cing Gyr Depression2	21.0

Panel 1.2 Summary: Ag1216 The MOL4 gene is well expressed in a variety of normal tissues including kidney, heart, brain, thymus and lung. Of interest is the robust expression in activated endothelial cells, which may indicate that this gene is important for angiogenesis or lymphocyte trafficking. Inflammatory lymphocytes preferentially traffic into tissues by crossing activated endothelium. Expression of the MOL4 gene appears to be up regulated in renal cell carcinomas. In contrast, expression of the MOL4 gene is down regulated in a number of cancer cell lines (including pancreatic, CNS, breast, and lung) relative to the normal controls. No expression of this gene is detected in a variety of melanoma cell lines. Therefore, modulation of MOL4 gene function may provide an effective treatment for a variety of cancers.

Panel 2.2 Summary: Ag1216 Expression of the MOL4 gene appears to be associated with kidney cancers. This is in good agreement with the data obtained in Panel 1.2 and

suggests that therapeutic modulation of this gene using inhibitory monoclonal antibodies or small molecules may prove useful in the treatment of kidney cancers. In addition, the MOL4 gene may be a useful marker for the detection of renal cell carcinomas.

Panel 4D Summary: Ag1216 Two replicate experiments using the same probe and primer set were in good agreement. The MOL4 transcript is highly expressed in thymus. To a much lesser degree, the transcript is also expressed in the lung as well as in small airway epithelium treated with TNF- α and IL-1 β . Therefore, protein therapeutics designed against the protein encoded for by this transcript could reduce inflammation in asthma or other lung disease such as emphysema.

Panel CNSD.01 Summary: Ag1216 Semaphorins can act as axon guidance proteins, specifically through their ability to act as chemorepellents that inhibit CNS regenerative capacity. Manipulation of levels of the MOL4 semaphorin-like protein may therefore be of use in inducing a compensatory synaptogenic response to neuronal death in Alzheimer's disease, Parkinson's disease, Huntington's disease, spinocerebellar ataxia, progressive supranuclear palsy, multiple sclerosis, ALS, head trauma, stroke, or any other disease/condition associated with neuronal loss.

E. MOL5a

Expression of gene MOL5a was assessed using the primer-probe sets Ag1215 and Ag1382 (identical sequences), described in Tables 33 and 34. Results of the RTQ-PCR runs are shown in Tables 35, 36, and 37.

Table 33. Probe Name Ag1215/Ag1382

Primers	Sequences	TM	Length	Start Position	SEQ ID NO:
Forward	5'-AACCCATTATCCTGCGTAACAT-3'	59.6	22	619	80
Probe	FAM-5'- CCCCACCACTCCATGAAGACAGAGTA-3'- TAMRA	68.5	26	645	81
Reverse	5'-CCTACAAAGTGAGGTTCGTTGA-3'	59.3	22	685	82

Table 34. Panel 1.2

Tissue Name	Relative Expression(%)	Relative Expression(%)
-------------	------------------------	------------------------

	1.2tm1403f_ ag1215	1.2tm1581t_ ag1382
Endothelial cells	21.9	17.3
Endothelial cells (treated)	100.0	40.9
Pancreas	14.7	0.4
Pancreatic ca. CAPAN 2	3.4	0.7
Adrenal Gland (new lot*)	26.4	10.4
Thyroid	18.8	0.3
Salivary gland	21.5	5.8
Pituitary gland	23.8	1.4
Brain (fetal)	33.9	1.4
Brain (whole)	69.3	3.8
Brain (amygdala)	13.9	3.6
Brain (cerebellum)	67.4	3.0
Brain (hippocampus)	45.1	12.6
Brain (thalamus)	19.1	26.4
Cerebral Cortex	53.2	30.1
Spinal cord	45.4	7.2
CNS ca. (glio/astro) U87-MG	7.8	21.3
CNS ca. (glio/astro) U-118-MG	6.8	13.5
CNS ca. (astro) SW1783	2.0	1.8
CNS ca.* (neuro; met) SK-N-AS	50.3	27.5
CNS ca. (astro) SF-539	20.3	21.2
CNS ca. (astro) SNB-75	13.7	2.8
CNS ca. (glio) SNB-19	19.5	28.9
CNS ca. (glio) U251	15.2	0.0
CNS ca. (glio) SF-295	15.0	5.1
Heart	63.3	12.2
Skeletal Muscle (new lot*)	27.7	0.8
Bone marrow	2.9	0.9
Thymus	4.3	2.8
Spleen	33.4	15.6
Lymph node	23.7	5.4
Colorectal	8.4	2.4
Stomach	36.3	9.6
Small intestine	27.9	11.7
Colon ca. SW480	6.1	1.8
Colon ca.* (SW480 met)SW620	10.4	40.3
Colon ca. HT29	3.0	2.5
Colon ca. HCT-116	6.9	11.0
Colon ca. CaCo-2	13.1	28.9
83219 CC Well to Mod Diff (ODO3866)	3.1	1.8
Colon ca. HCC-2998	12.6	9.5
Gastric ca.* (liver met) NCI-N87	18.4	17.6
Bladder	40.1	15.5

Trachea	13.8	6.0
Kidney	19.5	42.9
Kidney (fetal)	30.4	61.6
Renal ca. 786-0	6.1	6.7
Renal ca. A498	13.0	9.3
Renal ca. RXF 393	8.4	6.0
Renal ca. ACHN	10.7	4.9
Renal ca. UO-31	8.8	3.6
Renal ca. TK-10	15.4	6.2
Liver	15.2	3.2
Liver (fetal)	13.3	5.9
Liver ca. (hepatoblast) HepG2	21.8	12.1
Lung	19.3	0.7
Lung (fetal)	28.1	4.5
Lung ca. (small cell) LX-1	24.5	24.0
Lung ca. (small cell) NCI-H69	8.1	12.7
Lung ca. (s.cell var.) SHP-77	3.8	1.8
Lung ca. (large cell) NCI-H460	40.3	19.5
Lung ca. (non-sm. cell) A549	13.1	13.9
Lung ca. (non-s.cell) NCI-H23	28.1	24.5
Lung ca. (non-s.cell) HOP-62	42.3	9.7
Lung ca. (non-s.cl) NCI-H522	90.1	44.1
Lung ca. (squam.) SW 900	37.4	57.8
Lung ca. (squam.) NCI-H596	9.8	4.2
Mammary gland	42.6	9.0
Breast ca.* (pl. effusion) MCF-7	85.3	56.6
Breast ca.* (pl.ef) MDA-MB-231	5.3	1.4
Breast ca.* (pl. effusion) T47D	5.6	16.6
Breast ca. BT-549	5.0	2.6
Breast ca. MDA-N	16.7	3.7
Ovary	49.0	23.0
Ovarian ca. OVCAR-3	46.3	50.7
Ovarian ca. OVCAR-4	11.3	10.6
Ovarian ca. OVCAR-5	28.5	66.9
Ovarian ca. OVCAR-8	19.8	100.0
Ovarian ca. IGROV-1	18.2	13.3
Ovarian ca.* (ascites) SK-OV-3	25.7	10.3
Uterus	24.5	3.5
Placenta	90.1	82.9
Prostate	28.5	15.0
Prostate ca.* (bone met) PC-3	39.0	15.4
Testis	8.4	0.6
Melanoma Hs688(A).T	3.8	1.2
Melanoma* (met) Hs688(B).T	2.9	0.8
Melanoma UACC-62	23.2	11.4

Melanoma M14	13.7	6.7
Melanoma LOX IMVI	9.6	1.8
Melanoma* (met) SK-MEL-5	27.4	8.9
Adipose	6.2	12.8

Table 35. Panel 2.2

Tissue Name	Relative Expression(%)	Tissue Name	Relative Expression(%)
	2.2x4tm6515f_ag1215_a2		2.2x4tm6515f_ag1215_a2
Normal Colon GENPAK 061003	31.4	83793 Kidney NAT (OD04348)	39.7
97759 Colon cancer (OD06064)	34.3	98938 Kidney malignant cancer (OD06204B)	15.4
97760 Colon cancer NAT (OD06064)	18.6	98939 Kidney normal adjacent tissue (OD06204E)	10.4
97778 Colon cancer (OD06159)	2.7	85973 Kidney Cancer (OD04450-01)	15.3
97779 Colon cancer NAT (OD06159)	22.5	85974 Kidney NAT (OD04450-03)	20.3
98861 Colon cancer (OD06297-04)	3.2	Kidney Cancer Clontech 8120613	1.4
98862 Colon cancer NAT (OD06297-015)	30.6	Kidney NAT Clontech 8120614	20.3
83237 CC Gr.2 ascend colon (ODO3921)	11.6	Kidney Cancer Clontech 9010320	10.5
83238 CC NAT (ODO3921)	8.4	Kidney NAT Clontech 9010321	9.0
97766 Colon cancer metastasis (OD06104)	5.1	Kidney Cancer Clontech 8120607	32.2
97767 Lung NAT (OD06104)	8.3	Kidney NAT Clontech 8120608	12.1
87472 Colon mets to lung (OD04451-01)	15.3	Normal Uterus GENPAK 061018	31.8
87473 Lung NAT (OD04451-02)	4.3	Uterus Cancer GENPAK 064011	31.4
Normal Prostate Clontech A+ 6546-1 (8090438)	11.2	Normal Thyroid Clontech A+ 6570-1 (7080817)	3.0
84140 Prostate Cancer (OD04410)	10.0	Thyroid Cancer GENPAK 064010	14.8
84141 Prostate NAT (OD04410)	14.3	Thyroid Cancer INVITROGEN A302152	37.7
Normal Ovary Res. Gen.	74.7	Thyroid NAT INVITROGEN A302153	7.0
98863 Ovarian cancer (OD06283-03)	27.6	Normal Breast GENPAK 061019	35.4
98865 Ovarian cancer NAT/fallopian tube (OD06283-07)	6.4	84877 Breast Cancer (OD04566)	15.6
Ovarian Cancer GENPAK	16.2	Breast Cancer Res. Gen. 1024	51.4

064008			
97773 Ovarian cancer (OD06145)	8.8	85975 Breast Cancer (OD04590-01)	36.8
97775 Ovarian cancer NAT (OD06145)	24.6	85976 Breast Cancer Mets (OD04590-03)	21.0
98853 Ovarian cancer (OD06455-03)	9.9	87070 Breast Cancer Metastasis (OD04655-05)	66.6
98854 Ovarian NAT (OD06455-07) Fallopian tube	12.9	GENPAK Breast Cancer 064006	19.0
Normal Lung GENPAK 061010	18.0	Breast Cancer Clontech 9100266	27.7
92337 Invasive poor diff. lung adeno (ODO4945-01)	11.8	Breast NAT Clontech 9100265	21.6
92338 Lung NAT (ODO4945-03)	13.8	Breast Cancer INVITROGEN A209073	15.1
84136 Lung Malignant Cancer (OD03126)	31.7	Breast NAT INVITROGEN A2090734	28.5
84137 Lung NAT (OD03126)	5.6	97763 Breast cancer (OD06083)	100.0
90372 Lung Cancer (OD05014A)	17.7	97764 Breast cancer node metastasis (OD06083)	64.9
90373 Lung NAT (OD05014B)	13.7	Normal Liver GENPAK 061009	17.1
97761 Lung cancer (OD06081)	10.2	Liver Cancer Research Genetics RNA 1026	15.0
97762 Lung cancer NAT (OD06081)	8.2	Liver Cancer Research Genetics RNA 1025	36.3
85950 Lung Cancer (OD04237-01)	15.0	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	18.1
85970 Lung NAT (OD04237-02)	24.0	Paired Liver Tissue Research Genetics RNA 6004-N	6.5
83255 Ocular Mel Met to Liver (ODO4310)	25.5	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	33.3
83256 Liver NAT (ODO4310)	18.1	Paired Liver Tissue Research Genetics RNA 6005-N	31.6
84139 Melanoma Mets to Lung (OD04321)	41.3	Liver Cancer GENPAK 064003	8.9
84138 Lung NAT (OD04321)	9.1	Normal Bladder GENPAK 061001	14.7
Normal Kidney GENPAK 061008	7.5	Bladder Cancer Research Genetics RNA 1023	6.0
83786 Kidney Ca, Nuclear grade 2 (OD04338)	34.7	Bladder Cancer INVITROGEN A302173	28.9
83787 Kidney NAT (OD04338)	7.6	Normal Stomach GENPAK 061017	33.6
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	38.3	Gastric Cancer Clontech 9060397	3.6
83789 Kidney NAT (OD04339)	6.8	NAT Stomach Clontech 9060396	12.2
83790 Kidney Ca, Clear cell type (OD04340)	19.2	Gastric Cancer Clontech 9060395	15.1

83791 Kidney NAT (OD04340)	18.7	NAT Stomach Clontech 9060394	21.2
83792 Kidney Ca, Nuclear grade 3 (OD04348)	10.4	Gastric Cancer GENPAK 064005	17.4

Panel 36. Panel 4D

Tissue Name	Relative Expression(%)	Relative Expression(%)
	4Dtm2070f_ ag1215	4Dtm2425t_ ag1382
93768 Secondary Th1 anti-CD28/anti-CD3	27.9	19.6
93769 Secondary Th2 anti-CD28/anti-CD3	35.4	25.5
93770 Secondary Tr1 anti-CD28/anti-CD3	42.0	37.6
93573 Secondary Th1 resting day 4-6 in IL-2	29.5	18.8
93572 Secondary Th2 resting day 4-6 in IL-2	27.5	21.9
93571 Secondary Tr1 resting day 4-6 in IL-2	33.7	23.2
93568 primary Th1 anti-CD28/anti-CD3	35.1	28.1
93569 primary Th2 anti-CD28/anti-CD3	31.4	25.7
93570 primary Tr1 anti-CD28/anti-CD3	55.9	42.6
93565 primary Th1 resting dy 4-6 in IL-2	91.4	100.0
93566 primary Th2 resting dy 4-6 in IL-2	68.8	64.6
93567 primary Tr1 resting dy 4-6 in IL-2	55.5	52.1
93351 CD45RA CD4 lymphocyte anti-CD28/anti-CD3	21.6	17.8
93352 CD45RO CD4 lymphocyte anti-CD28/anti-CD3	24.5	17.2
93251 CD8 Lymphocytes anti-CD28/anti-CD3	22.1	15.5
93353 chronic CD8 Lymphocytes 2ry resting dy 4-6 in IL-2	17.1	12.4
93574 chronic CD8 Lymphocytes 2ry activated CD3/CD28	29.7	18.2
93354 CD4 none	17.9	15.4
93252 Secondary Th1/Th2/Tr1 anti-CD95 CH11	71.7	67.4
93103 LAK cells resting	17.1	10.3
93788 LAK cells IL-2	21.5	15.7
93787 LAK cells IL-2+IL-12	18.4	17.1
93789 LAK cells IL-2+IFN gamma	29.5	22.2
93790 LAK cells IL-2+ IL-18	18.0	22.1
93104 LAK cells PMA/ionomycin and IL-18	10.7	7.3
93578 NK Cells IL-2 resting	31.9	17.2
93109 Mixed Lymphocyte Reaction Two Way MLR	9.5	7.6
93110 Mixed Lymphocyte Reaction Two Way MLR	6.2	6.8
93111 Mixed Lymphocyte Reaction Two Way MLR	10.5	8.5
93112 Mononuclear Cells (PBMCs) resting	10.7	10.3
93113 Mononuclear Cells (PBMCs) PWM	50.7	38.4
93114 Mononuclear Cells (PBMCs) PHA-L	32.5	31.2
93249 Ramos (B cell) none	0.0	0.0

93250_Ramos (B cell)_ionomycin	0.0	0.0
93349_B lymphocytes PWM	36.1	34.2
93350_B lymphocytes CD40L and IL-4	18.3	17.2
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	43.8	30.1
93248_EOL-1 (Eosinophil)_dbcAMP/PMA/ionomycin	73.2	63.7
93356_Dendritic Cells_none	1.6	0.6
93355_Dendritic Cells_LPS 100 ng/ml	1.2	5.0
93775_Dendritic Cells_anti-CD40	0.9	0.9
93774_Monocytes_resting	2.9	1.8
93776_Monocytes_LPS 50 ng/ml	29.7	19.2
93581_Macrophages_resting	4.9	2.3
93582_Macrophages_LPS 100 ng/ml	7.2	4.4
93098_HUVEC (Endothelial)_none	9.2	6.5
93099_HUVEC (Endothelial)_starved	18.6	14.7
93100_HUVEC (Endothelial)_IL-1b	3.9	2.6
93779_HUVEC (Endothelial)_IFN gamma	19.2	17.1
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	2.1	2.4
93101_HUVEC (Endothelial)_TNF alpha + IL4	15.3	12.2
93781_HUVEC (Endothelial)_IL-11	13.6	15.3
93583_Lung Microvascular Endothelial Cells_none	19.9	20.4
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	18.0	14.9
92662_Microvascular Dermal endothelium_none	29.7	26.8
92663_Microvascular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	36.9	33.4
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	41.5	25.7
93347_Small Airway Epithelium_none	13.3	8.8
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	56.6	45.4
92668_Coronary Artery SMC_resting	22.2	19.8
92669_Coronary Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	28.1	19.9
93107_astrocytes_resting	13.0	20.2
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	23.7	18.6
92666_KU-812 (Basophil)_resting	97.3	75.3
92667_KU-812 (Basophil)_PMA/ionomycin	100.0	90.1
93579_CCD1106 (Keratinocytes)_none	16.6	13.8
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	67.8	11.3
93791_Liver Cirrhosis	14.3	12.3
93792_Lupus Kidney	28.7	18.8
93577_NCI-H292	27.4	28.3
93358_NCI-H292_IL-4	61.1	55.1
93360_NCI-H292_IL-9	37.6	31.6
93359_NCI-H292_IL-13	44.4	42.9
93357_NCI-H292_IFN gamma	21.0	20.3
93777_HPAEC_-	21.5	17.2

93778_HPAEC_IL-1 beta/TNA alpha	11.0	9.5
93254_Normal Human Lung Fibroblast_none	31.0	20.6
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	26.1	23.5
93257_Normal Human Lung Fibroblast_IL-4	40.6	37.1
93256_Normal Human Lung Fibroblast_IL-9	21.3	17.7
93255_Normal Human Lung Fibroblast_IL-13	56.3	53.2
93258_Normal Human Lung Fibroblast_IFN gamma	59.5	45.4
93106_Dermal Fibroblasts CCD1070_resting	47.0	33.4
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	73.7	55.1
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	36.6	37.4
93772_dermal fibroblast_IFN gamma	8.8	9.7
93771_dermal fibroblast_IL-4	20.2	19.6
93259_IBD Colitis 1**	13.2	10.7
93260_IBD Colitis 2	4.1	2.0
93261_IBD Crohns	3.1	3.1
735010_Colon normal	29.9	24.3
735019_Lung_none	46.0	38.4
64028-1_Thymus_none	60.3	54.0
64030-1_Kidney_none	32.1	26.4

Table 37. Panel CNSD.01

Tissue Name	Relative Expression(%) cns1x4tm6177f ag1215 b1	Tissue Name	Relative Expression(%) cns1x4tm6177f ag1215 b1
102633_BA4 Control	20.2	102605_BA17 PSP	31.1
102641_BA4 Control2	34.5	102612_BA17 PSP2	9.9
102625_BA4 Alzheimer's2	9.0	102637_Sub Nigra Control	54.5
102649_BA4 Parkinson's	32.9	102645_Sub Nigra Control2	31.7
102656_BA4 Parkinson's2	46.8	102629_Sub Nigra Alzheimer's2	24.2
102664_BA4 Huntington's	36.2	102660_Sub Nigra Parkinson's2	91.5
102671_BA4 Huntington's2	11.1	102667_Sub Nigra Huntington's	80.6
102603_BA4 PSP	15.8	102674_Sub Nigra Huntington's2	43.0
102610_BA4 PSP2	45.9	102614_Sub Nigra PSP2	24.8
102588_BA4 Depression	19.6	102592_Sub Nigra Depression	18.5
102596_BA4 Depression2	7.8	102599_Sub Nigra Depression2	12.0
102634_BA7 Control	26.1	102636_Glob Palladus Control	20.2
102642_BA7 Control2	32.8	102644_Glob Palladus Control2	10.7
102626_BA7 Alzheimer's2	4.5	102620_Glob Palladus Alzheimer's	21.6
102650_BA7 Parkinson's	22.9	102628_Glob Palladus Alzheimer's2	4.9

102657_BA7 Parkinson's2	35.5	102652_Glob Palladus Parkinson's	100.0
102665_BA7 Huntington's	39.1	102659_Glob Palladus Parkinson's2	23.0
102672_BA7 Huntington's2	40.4	102606_Glob Palladus PSP	10.1
102604_BA7 PSP	31.2	102613_Glob Palladus PSP2	11.8
102611_BA7 PSP2	32.2	102591_Glob Palladus Depression	23.4
102589_BA7 Depression	6.2	102638_Temp Pole Control	7.7
102632_BA9 Control	12.5	102646_Temp Pole Control2	29.2
102640_BA9 Control2	48.5	102622_Temp Pole Alzheimer's	4.0
102617_BA9 Alzheimer's	6.9	102630_Temp Pole Alzheimer's2	3.6
102624_BA9 Alzheimer's2	5.4	102653_Temp Pole Parkinson's	22.5
102648_BA9 Parkinson's	25.2	102661_Temp Pole Parkinson's2	22.1
102655_BA9 Parkinson's2	33.4	102668_Temp Pole Huntington's	30.6
102663_BA9 Huntington's	44.8	102607_Temp Pole PSP	3.8
102670_BA9 Huntington's2	13.7	102615_Temp Pole PSP2	2.2
102602_BA9 PSP	23.4	102600_Temp Pole Depression2	7.1
102609_BA9 PSP2	5.0	102639_Cing Gyr Control	58.9
102587_BA9 Depression	10.8	102647_Cing Gyr Control2	40.2
102595_BA9 Depression2	11.8	102623_Cing Gyr Alzheimer's	19.3
102635_BA17 Control	39.6	102631_Cing Gyr Alzheimer's2	11.8
102643_BA17 Control2	40.0	102654_Cing Gyr Parkinson's	42.1
102627_BA17 Alzheimer's2	7.6	102662_Cing Gyr Parkinson's2	35.7
102651_BA17 Parkinson's	31.2	102669_Cing Gyr Huntington's	62.0
102658_BA17 Parkinson's2	35.2	102676_Cing Gyr Huntington's2	28.7
102666_BA17 Huntington's	47.2	102608_Cing Gyr PSP	66.8
102673_BA17 Huntington's2	25.0	102616_Cing Gyr PSP2	5.2
102590_BA17 Depression	22.2	102594_Cing Gyr Depression	14.7
102597_BA17 Depression2	41.7	102601_Cing Gyr Depression2	32.0

Panel 1.2 Summary: Ag1215/Ag1382 Two replicate experiments were performed using probe and primer sets of identical sequences; however, relatively disparate results were obtained on this panel. For Ag1215, the MOL5a gene is expressed at high levels across most of the tissues on this panel with highest expression in treated endothelial cells (CT value = 23). For Ag1382, the MOL5a gene is expressed at high levels across most of the tissues on this panel with highest expression in an ovarian cancer cell line (CT value = 22). To summarize the expression profile, there appears to be widespread expression of the MOL5a gene in a number of tissues and cell lines. Furthermore, the expression of this gene seems to be associated with reproductive tissues and cancer cell lines whose origins are such. For

instance, there is significant expression in ovarian cell lines, breast cell lines and placenta tissue. There is also moderate expression in kidney tissues and lung cell lines.

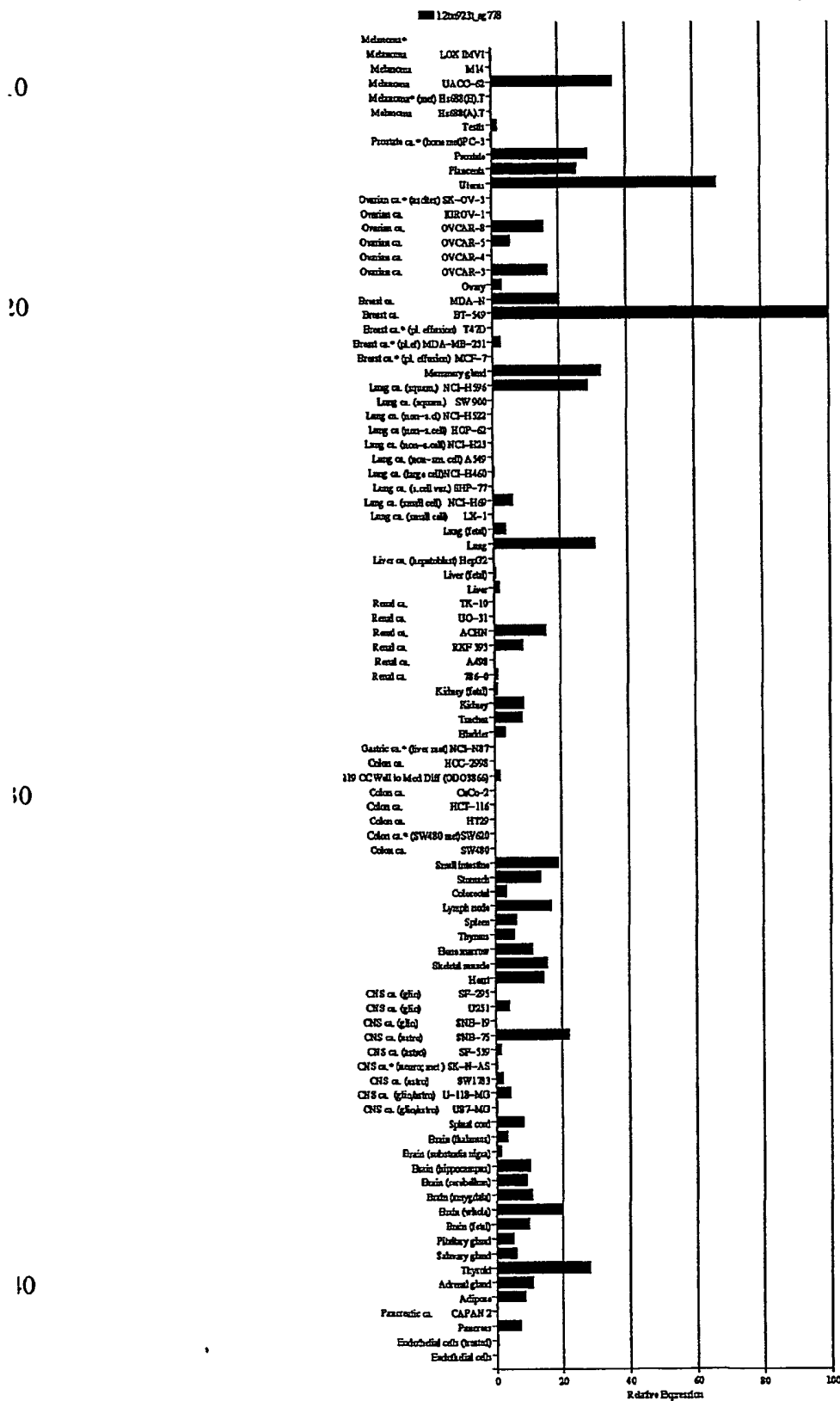
Panel 2.2 Summary: Ag1215 There appears to be widespread expression of the MOL5a gene in the samples of panel 2.2. Specifically, there seems to be an association of expression in breast cancer and normal ovarian tissue. This is reasonably consistent with the results obtained from Panel 1.2. In addition, there is also some correlation with expression in normal kidney tissue when compared to kidney cancers, also consistent with the observations in Panel 1.2. Thus, therapeutic modulation of this gene or gene product might show utility in the treatment of breast cancer, ovarian cancer or kidney cancer.

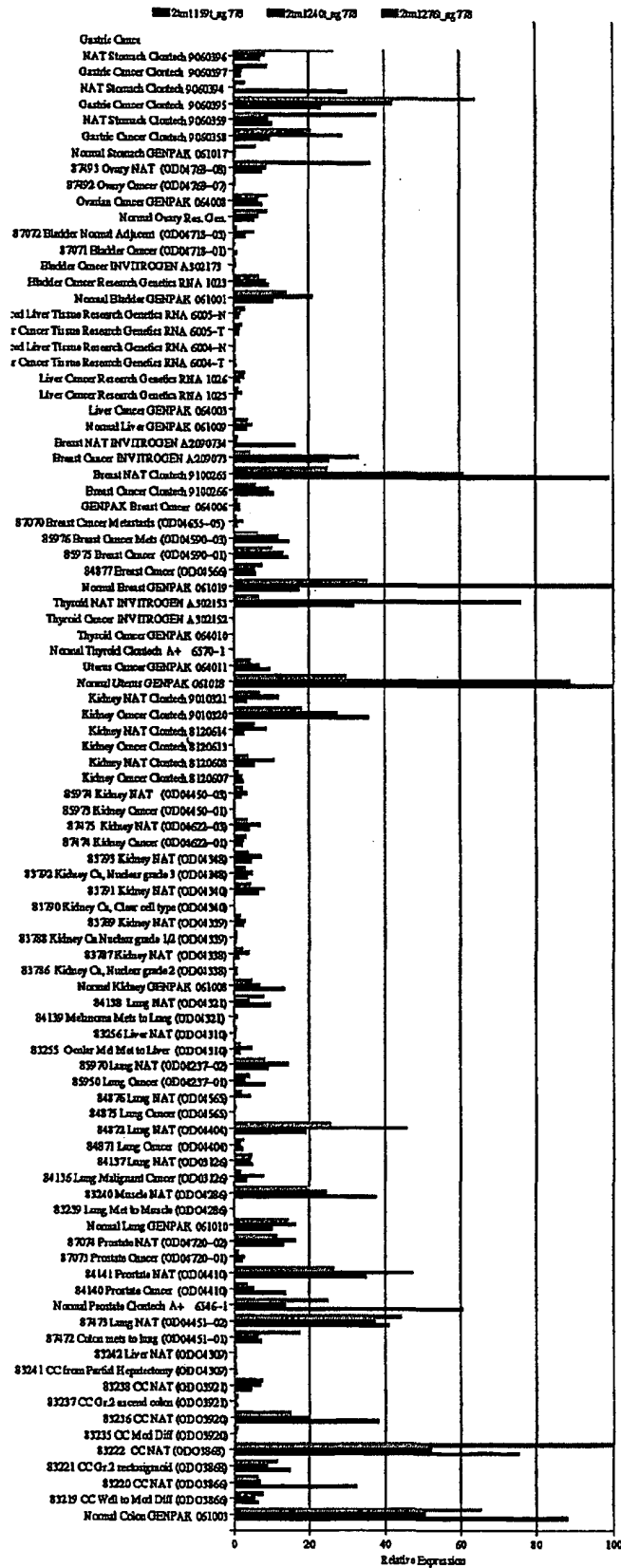
Panel 4D Summary: Ag1215/Ag1382 Results from two replicate experiments performed using probe and primer sets of identical sequences are in reasonable agreement. The MOL5a transcript is widely expressed in cell lines from this panel (CT values = 25-30), including thymus, lung, muco-epidermoid cell lines, fibroblasts from diverse origin, and activated T cells. In addition, the MOL5a gene is expressed in normal colon but not in colons from patients with Crohn's disease or colitis. Thus, protein therapeutics designed with the putative semaphorin encoded for by this protein could reduce or eliminate inflammation and tissue destruction due to IBD. High expression of this transcript was found on primary resting Th1 T cells, and also primary resting Th2 and Tr1 T cells. The high expression of this transcript in secondary T cells treated with CD95 suggests that this transcript encodes for a protein involved in activation of cell death. Furthermore, high expression of the MOL5A transcript is also found in activated basophils and eosinophils, suggesting a role for this protein in allergic disorder such as asthma, contact hypersensitivity, and hypersensitive immediate reactions. Antibody or protein therapeutics designed against the protein encoded for by this transcript could therefore reduce or inhibit inflammation in allergy, asthma, emphysema, psoriasis and/or autoimmunity.

Panel CNSD.01 Summary: Ag1215 Semaphorins can act as axon guidance proteins, specifically through their ability to act as chemorepellents that inhibit CNS regenerative capacity. Manipulation of levels of the MOL4 semaphorin-like protein may therefore be of use in inducing a compensatory synaptogenic response to neuronal death in Alzheimer's disease, Parkinson's disease, Huntington's disease, spinocerebellar ataxia, progressive supranuclear palsy, multiple sclerosis, ALS, head trauma, stroke, or any other disease/condition associated with neuronal loss.

Example 2: TaqMan Data for MOL7

TaqMan data was acquired for MOL7 as described in Example 1 using the primers specified. The relative expression of MOL7 in the described tissues is represented in the graphs below.





Example 3 SeqCalling™ Technology

cDNA was derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, cell lines, primary cells or tissue cultured primary cells and cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression for example, growth factors, chemokines, steroids. The cDNA thus derived was then sequenced using CuraGen's proprietary SeqCalling technology. Sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled with themselves and with public ESTs using bioinformatics programs to generate CuraGen's human SeqCalling database of SeqCalling assemblies. Each assembly contains one or more overlapping cDNA sequences derived from one or more human samples. Fragments and ESTs were included as components for an assembly when the extent of identity with another component of the assembly was at least 95% over 50 bp. Each assembly can represent a gene and/or its variants such as splice forms and/or single nucleotide polymorphisms (SNPs) and their combinations.

Variant sequences are included in this application. A variant sequence can include a single nucleotide polymorphism (SNP). A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA. A SNP can arise in several ways. For example, a SNP may be due to a substitution of one nucleotide for another at the polymorphic site. Such a substitution can be either a transition or a transversion. A SNP can also arise from a deletion of a nucleotide or an insertion of a nucleotide, relative to a reference allele. In this case, the polymorphic site is a site at which one allele bears a gap with respect to a particular nucleotide in another allele. SNPs occurring within genes may result in an alteration of the amino acid encoded by the gene at the position of the SNP. Intragenic SNPs may also be silent, however, in the case that a codon including a SNP encodes the same amino acid as a result of the redundancy of the genetic code. SNPs occurring outside the region of a gene, or in an intron within a gene, do not result in changes in any amino acid sequence of a protein but may result in altered regulation of the expression pattern for example, alteration in temporal expression, physiological response regulation, cell type expression regulation, intensity of expression, stability of transcribed message.

Method of novel SNP Identification: SNPs are identified by analyzing sequence assemblies using CuraGen's proprietary SNPTool algorithm. SNPTool identifies variation in assemblies with the following criteria: SNPs are not analyzed within 10 base pairs on both

ends of an alignment; Window size (number of bases in a view) is 10; The allowed number of mismatches in a window is 2; Minimum SNP base quality (PHRED score) is 23; Minimum number of changes to score an SNP is 2/assembly position. SNPTool analyzes the assembly and displays SNP positions, associated individual variant sequences in the assembly, the depth of the assembly at that given position, the putative assembly allele frequency, and the SNP sequence variation. Sequence traces are then selected and brought into view for manual validation. The consensus assembly sequence is imported into CuraTools along with variant sequence changes to identify potential amino acid changes resulting from the SNP sequence variation. Comprehensive SNP data analysis is then exported into the SNPCalling database.

Method of novel SNP Confirmation: SNPs are confirmed employing a validated method known as Pyrosequencing (Pyrosequencing, Westborough, MA). Detailed protocols for Pyrosequencing can be found in:

Alderborn et al. Determination of Single Nucleotide Polymorphisms by Real-time Pyrophosphate DNA Sequencing. (2000). Genome Research. 10, Issue 8, August. 1249-1265.

In brief, Pyrosequencing is a real time primer extension process of genotyping. This protocol takes double-stranded, biotinylated PCR products from genomic DNA samples and binds them to streptavidin beads. These beads are then denatured producing single stranded bound DNA. SNPs are characterized utilizing a technique based on an indirect bioluminometric assay of pyrophosphate (PPi) that is released from each dNTP upon DNA chain elongation. Following Klenow polymerase-mediated base incorporation, PPi is released and used as a substrate, together with adenosine 5'-phosphosulfate (APS), for ATP sulfurylase, which results in the formation of ATP. Subsequently, the ATP accomplishes the conversion of luciferin to its oxi-derivative by the action of luciferase. The ensuing light output becomes proportional to the number of added bases, up to about four bases. To allow processivity of the method dNTP excess is degraded by apyrase, which is also present in the starting reaction mixture, so that only dNTPs are added to the template during the sequencing. The process has been fully automated and adapted to a 96-well format, which allows rapid screening of large SNP panels.

EQUIVALENTS

Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims, which follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. The choice of nucleic acid starting material, clone of interest, or library type is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein. Other aspects, advantages, and modifications considered to be within the scope of the following claims.

WHAT IS CLAIMED IS:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:
 - (a) a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24;
 - (b) a variant of a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of the amino acid residues from the amino acid sequence of said mature form;
 - (c) an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24; and
 - (d) a variant of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence.
2. The polypeptide of claim 1, wherein said polypeptide comprises the amino acid sequence of a naturally-occurring allelic variant of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24.
3. The polypeptide of claim 2, wherein said allelic variant comprises an amino acid sequence that is the translation of a nucleic acid sequence differing by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23.
4. The polypeptide of claim 1, wherein the amino acid sequence of said variant comprises a conservative amino acid substitution.

5. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of:
 - (a) a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24;
 - (b) a variant of a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of the amino acid residues from the amino acid sequence of said mature form;
 - (c) an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24;
 - (d) a variant of an amino acid sequence selected from the group consisting SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence;
 - (e) a nucleic acid fragment encoding at least a portion of a polypeptide comprising an amino acid sequence chosen from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, or a variant of said polypeptide, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence; and
 - (f) a nucleic acid molecule comprising the complement of (a), (b), (c), (d) or (e).
6. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule comprises the nucleotide sequence of a naturally-occurring allelic nucleic acid variant.
7. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule encodes a polypeptide comprising the amino acid sequence of a naturally-occurring polypeptide variant.

8. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule differs by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23.
9. The nucleic acid molecule of claim 5, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of:
 - (a) a nucleotide sequence selected from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23;
 - (b) a nucleotide sequence differing by one or more nucleotides from a nucleotide sequence selected from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23, provided that no more than 20% of the nucleotides differ from said nucleotide sequence;
 - (c) a nucleic acid fragment of (a); and
 - (d) a nucleic acid fragment of (b).
10. The nucleic acid molecule of claim 5, wherein said nucleic acid molecule hybridizes under stringent conditions to a nucleotide sequence chosen from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, and 23, or a complement of said nucleotide sequence.
11. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of:
 - (a) a first nucleotide sequence comprising a coding sequence differing by one or more nucleotide sequences from a coding sequence encoding said amino acid sequence, provided that no more than 20% of the nucleotides in the coding sequence in said first nucleotide sequence differ from said coding sequence;
 - (b) an isolated second polynucleotide that is a complement of the first polynucleotide; and
 - (c) a nucleic acid fragment of (a) or (b).
12. A vector comprising the nucleic acid molecule of claim 11.
13. The vector of claim 12, further comprising a promoter operably-linked to said nucleic acid molecule.

14. A cell comprising the vector of claim 12.
15. An antibody that binds immunospecifically to the polypeptide of claim 1.
16. The antibody of claim 15, wherein said antibody is a monoclonal antibody.
17. The antibody of claim 15, wherein the antibody is a humanized antibody.
18. A method for determining the presence or amount of the polypeptide of claim 1 in a sample, the method comprising:
 - (a) providing the sample;
 - (b) contacting the sample with an antibody that binds immunospecifically to the polypeptide; and
 - (c) determining the presence or amount of antibody bound to said polypeptide,thereby determining the presence or amount of polypeptide in said sample.
19. A method for determining the presence or amount of the nucleic acid molecule of claim 5 in a sample, the method comprising:
 - (a) providing the sample;
 - (b) contacting the sample with a probe that binds to said nucleic acid molecule; and
 - (c) determining the presence or amount of the probe bound to said nucleic acid molecule,thereby determining the presence or amount of the nucleic acid molecule in said sample.
20. The method of claim 19 wherein presence or amount of the nucleic acid molecule is used as a marker for cell or tissue type.
21. The method of claim 20 wherein the cell or tissue type is cancerous.
22. A method of identifying an agent that binds to a polypeptide of claim 1, the method comprising:
 - (a) contacting said polypeptide with said agent; and
 - (b) determining whether said agent binds to said polypeptide.

23. The method of claim 22 wherein the agent is a cellular receptor or a downstream effector.
24. A method for identifying an agent that modulates the expression or activity of the polypeptide of claim 1, the method comprising:
- (a) providing a cell expressing said polypeptide;
 - (b) contacting the cell with said agent, and
 - (c) determining whether the agent modulates expression or activity of said polypeptide,
- whereby an alteration in expression or activity of said peptide indicates said agent modulates expression or activity of said polypeptide.
25. A method for modulating the activity of the polypeptide of claim 1, the method comprising contacting a cell sample expressing the polypeptide of said claim with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptide.
26. A method of treating or preventing a MOLX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired the polypeptide of claim 1 in an amount sufficient to treat or prevent said MOLX-associated disorder in said subject.
27. The method of claim 26 wherein the disorder is selected from the group consisting of cardiomyopathy and atherosclerosis.
28. The method of claim 26 wherein the disorder is related to cell signal processing and metabolic pathway modulation.
29. The method of claim 26, wherein said subject is a human.
30. A method of treating or preventing a MOLX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired

the nucleic acid of claim 5 in an amount sufficient to treat or prevent said MOLX-associated disorder in said subject.

31. The method of claim 30 wherein the disorder is selected from the group consisting of cardiomyopathy and atherosclerosis.
32. The method of claim 30 wherein the disorder is related to cell signal processing and metabolic pathway modulation.
33. The method of claim 30, wherein said subject is a human.
34. A method of treating or preventing a MOLX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired the antibody of claim 15 in an amount sufficient to treat or prevent said MOLX-associated disorder in said subject.
35. The method of claim 34 wherein the disorder is diabetes.
36. The method of claim 34 wherein the disorder is related to cell signal processing and metabolic pathway modulation.
37. The method of claim 34, wherein the subject is a human.
38. A pharmaceutical composition comprising the polypeptide of claim 1 and a pharmaceutically-acceptable carrier.
39. A pharmaceutical composition comprising the nucleic acid molecule of claim 5 and a pharmaceutically-acceptable carrier.
40. A pharmaceutical composition comprising the antibody of claim 15 and a pharmaceutically-acceptable carrier.
41. A kit comprising in one or more containers, the pharmaceutical composition of claim 38.

42. A kit comprising in one or more containers, the pharmaceutical composition of claim
43. A kit comprising in one or more containers, the pharmaceutical composition of claim 4
44. A method for determining the presence of or predisposition to a disease associated with altered levels of the polypeptide of claim 1 in a first mammalian subject, the method comprising:
- (a) measuring the level of expression of the polypeptide in a sample from the first mammalian subject; and
 - (b) comparing the amount of said polypeptide in the sample of step (a) to the amount of the polypeptide present in a control sample from a second mammalian subject known not to have, or not to be predisposed to, said disease;
- wherein an alteration in the expression level of the polypeptide in the first subject as compared to the control sample indicates the presence of or predisposition to said disease.
45. The method of claim 44 wherein the predisposition is to cancers.
46. A method for determining the presence of or predisposition to a disease associated with altered levels of the nucleic acid molecule of claim 5 in a first mammalian subject, the method comprising:
- (a) measuring the amount of the nucleic acid in a sample from the first mammalian subject; and
 - (b) comparing the amount of said nucleic acid in the sample of step (a) to the amount of the nucleic acid present in a control sample from a second mammalian subject known not to have or not be predisposed to, the disease;
- wherein an alteration in the level of the nucleic acid in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.
47. The method of claim 46 wherein the predisposition is to a cancer.

48. A method of treating a pathological state in a mammal, the method comprising administering to the mammal a polypeptide in an amount that is sufficient to alleviate the pathological state, wherein the polypeptide is a polypeptide having an amino acid sequence at least 95% identical to a polypeptide comprising an amino acid sequence of at least one of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, or a biologically active fragment thereof.
49. A method of treating a pathological state in a mammal, the method comprising administering to the mammal the antibody of claim 15 in an amount sufficient to alleviate the pathological state.
50. A method for the screening of a candidate substance interacting with an olfactory receptor polypeptide selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, or fragments or variants thereof, comprises the following steps:
- a) providing a polypeptide selected from the group consisting of the sequences of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, or a peptide fragment or a variant thereof;
 - b) obtaining a candidate substance;
 - c) bringing into contact said polypeptide with said candidate substance;
 - and
 - d) detecting the complexes formed between said polypeptide and said candidate substance.
51. A method for the screening of ligand molecules interacting with an olfactory receptor polypeptide selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, wherein said method comprises:

- a) providing a recombinant eukaryotic host cell containing a nucleic acid encoding a polypeptide selected from the group consisting of the polypeptides comprising the amino acid sequences SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24;
 - b) preparing membrane extracts of said recombinant eukaryotic host cell;
 - c) bringing into contact the membrane extracts prepared at step b) with a selected ligand molecule; and
 - d) detecting the production level of second messengers metabolites.
52. A method for the screening of ligand molecules interacting with an olfactory receptor polypeptide selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24, wherein said method comprises:
- a) providing an adenovirus containing a nucleic acid encoding a polypeptide selected from the group consisting of polypeptides comprising the amino acid sequences SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24;
 - b) infecting an olfactory epithelium with said adenovirus;
 - c) bringing into contact the olfactory epithelium b) with a selected ligand molecule; and
 - d) detecting the increase of the response to said ligand molecule.

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